

=> file medline

FILE 'MEDLINE' ENTERED AT 12:07:23 ON 28 JUL 2003

FILE LAST UPDATED: 26 JUL 2003 (20030726/UP). FILE COVERS 1958 TO DATE.

On April 13, 2003, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See <http://www.nlm.nih.gov/mesh/changes2003.html> for a description on changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

CT = controlled terminology
 NT = narrower term
 BI = Biosynthesis
 IP = isolation & purification
 2 cites

=> d que 149

L43 37021 SEA FILE=MEDLINE ABB=ON PLU=ON CAROTENOIDS+NT/CT
 L44 82158 SEA FILE=MEDLINE ABB=ON PLU=ON OXYGEN/CT
 L47 1414 SEA FILE=MEDLINE ABB=ON PLU=ON L43(L)(BI OR IP)/CT
 L48 41 SEA FILE=MEDLINE ABB=ON PLU=ON L47 AND L44
 L49 2 SEA FILE=MEDLINE ABB=ON PLU=ON L48 AND (BIOGENESIS OR GIGANTEUS)/TI

=> file caba

FILE 'CABA' ENTERED AT 12:07:25 ON 28 JUL 2003
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FILE COVERS 1973 TO 7 Jul 2003 (20030707/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d que 167

L63 15147 SEA FILE=CABA ABB=ON PLU=ON CAROTEN?
 L64 884 SEA FILE=CABA ABB=ON PLU=ON L63 AND (CULTUR? OR FERMENT?)
 L65 8723 SEA FILE=CABA ABB=ON PLU=ON (OXYGEN? OR AEROB? OR O2 OR AERAT?)(5A)(VARY? OR CONTROL? OR LEVEL OR UPTAK? OR CONCENTRAT? OR AMOUNT)
 L66 7 SEA FILE=CABA ABB=ON PLU=ON L64 AND L65
 L67 1 SEA FILE=CABA ABB=ON PLU=ON L66 AND SUCCINATE/TI

=> file biotechno

FILE 'BIOTECHNO' ENTERED AT 12:07:26 ON 28 JUL 2003
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FILE LAST UPDATED: 22 JUL 2003 <20030722/UP>
 FILE COVERS 1980 TO DATE.

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN
 /CT AND BASIC INDEX <<<

=> d que 158

L53 2639 SEA FILE=BIOTECHNO ABB=ON PLU=ON ?CAROTEN?
 L54 393 SEA FILE=BIOTECHNO ABB=ON PLU=ON L53 AND (CULTUR? OR

FERMENT?)
 L55 73 SEA FILE=BIOTECHNO ABB=ON PLU=ON L54 AND (OXYGEN? OR AEROB?
 OR O2 OR AERAT?)
 L56 4620 SEA FILE=BIOTECHNO ABB=ON PLU=ON (OXYGEN? OR AEROB? OR O2 OR
 AERAT?)(5A)(VARY? OR CONTROL? OR CONCENTRAT? OR AMOUNT).
 L57 10 SEA FILE=BIOTECHNO ABB=ON PLU=ON L55 AND L56
 L58 3 SEA FILE=BIOTECHNO ABB=ON PLU=ON L57 AND (FOAM OR STOICHIOMET 3 cites
 RIC OR GLUT?)/TI

=> file hcaplus

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FILE COVERS 1907 - 28 Jul 2003 VOL 139 ISS 5
 FILE LAST UPDATED: 27 Jul 2003 (20030727/ED)



This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d que 118

L5 42 SEA FILE=REGISTRY ABB=ON PLU=ON (472-61-7/BI OR 4418-73-9/BI
 OR 144-68-3/BI OR 432-68-8/BI OR 4339-77-9/BI OR 4418-72-8/BI
 OR 514-78-3/BI OR 7235-40-7/BI OR 472-70-8/BI OR 108-20-3/BI
 OR 108-88-3/BI OR 108-94-1/BI OR 109-99-9/BI OR 110-54-3/BI OR
 110-82-7/BI OR 110-86-1/BI OR 116-30-3/BI OR 123-86-4/BI OR
 123-91-1/BI OR 1330-20-7/BI OR 141-78-6/BI OR 142-82-5/BI OR
 162875-45-8/BI OR 19866-02-5/BI OR 222713-29-3/BI OR 334071-56-
 6/BI OR 382660-64-2/BI OR 382660-65-3/BI OR 432-70-2/BI OR
 472-93-5/BI OR 502-65-8/BI OR 563-80-4/BI OR 60-29-7/BI OR
 64-17-5/BI OR 67-56-1/BI OR 67-64-1/BI OR 67-66-3/BI OR
 71-23-8/BI OR 71-43-2/BI OR 75-09-2/BI OR 7782-44-7/BI OR
 78-93-3/BI)
 L8 18 SEA FILE=REGISTRY ABB=ON PLU=ON L5 AND C6/ES
 L9 15 SEA FILE=REGISTRY ABB=ON PLU=ON L8 NOT 46.150.18/RID
 L10 1 SEA FILE=REGISTRY ABB=ON PLU=ON 7782-44-7
 L11 32232 SEA FILE=HCAPLUS ABB=ON PLU=ON CAROTENES+PFT,NT/CT
 L12 66957 SEA FILE=HCAPLUS ABB=ON PLU=ON L9
 L13 7229 SEA FILE=HCAPLUS ABB=ON PLU=ON (L11 OR L12)(L)PREP/RL
 L14 78324 SEA FILE=HCAPLUS ABB=ON PLU=ON FERMENTATION+PFT/CT
 L15 8976 SEA FILE=HCAPLUS ABB=ON PLU=ON CULTURE MEDIA +PFT/CT
 L16 373 SEA FILE=HCAPLUS ABB=ON PLU=ON L13 AND (L14 OR L15)
 L17 317219 SEA FILE=HCAPLUS ABB=ON PLU=ON L10
 L18 7 SEA FILE=HCAPLUS ABB=ON PLU=ON L16 AND L17 7 cites

*all carotenoids
in appl's citec*

*all of the
cpds indexed
in the cite
for applicants
priority docu-
ment*

*want cpds w/  ring
no  rings*

*PFT = old, new &
"used for" terms
preparative role*

=> d que 122

L5 42 SEA FILE=REGISTRY ABB=ON PLU=ON (472-61-7/BI OR 4418-73-9/BI OR 144-68-3/BI OR 432-68-8/BI OR 4339-77-9/BI OR 4418-72-8/BI OR 514-78-3/BI OR 7235-40-7/BI OR 472-70-8/BI OR 108-20-3/BI OR 108-88-3/BI OR 108-94-1/BI OR 109-99-9/BI OR 110-54-3/BI OR 110-82-7/BI OR 110-86-1/BI OR 116-30-3/BI OR 123-86-4/BI OR 123-91-1/BI OR 1330-20-7/BI OR 141-78-6/BI OR 142-82-5/BI OR 162875-45-8/BI OR 19866-02-5/BI OR 222713-29-3/BI OR 334071-56-6/BI OR 382660-64-2/BI OR 382660-65-3/BI OR 432-70-2/BI OR 472-93-5/BI OR 502-65-8/BI OR 563-80-4/BI OR 60-29-7/BI OR 64-17-5/BI OR 67-56-1/BI OR 67-64-1/BI OR 67-66-3/BI OR 71-23-8/BI OR 71-43-2/BI OR 75-09-2/BI OR 7782-44-7/BI OR 78-93-3/BI)

L8 18 SEA FILE=REGISTRY ABB=ON PLU=ON L5 AND C6/ES

L9 15 SEA FILE=REGISTRY ABB=ON PLU=ON L8 NOT 46.150.18/RID

L11 32232 SEA FILE=HCAPLUS ABB=ON PLU=ON CAROTENES+PFT,NT/CT

L12 66957 SEA FILE=HCAPLUS ABB=ON PLU=ON L9

L13 7229 SEA FILE=HCAPLUS ABB=ON PLU=ON (L11 OR L12)(L)PREP/RL

L14 78324 SEA FILE=HCAPLUS ABB=ON PLU=ON FERMENTATION+PFT/CT

L15 8976 SEA FILE=HCAPLUS ABB=ON PLU=ON CULTURE MEDIA +PFT/CT

L16 373 SEA FILE=HCAPLUS ABB=ON PLU=ON L13 AND (L14 OR L15)

L19 2187 SEA FILE=HCAPLUS ABB=ON PLU=ON BUBBLING/CT

L20 1915 SEA FILE=HCAPLUS ABB=ON PLU=ON AERATION/CT

L21 365 SEA FILE=HCAPLUS ABB=ON PLU=ON AERATORS/CT

L22 3 SEA FILE=HCAPLUS ABB=ON PLU=ON L16 AND (L19 OR L20 OR L21) 3 cites

=> s 118 or 122

L79 8 L18 OR L22 8 cites total for HCAPLUS

=> file wpix

FILE 'WPIX' ENTERED AT 12:07:30 ON 28 JUL 2003
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FILE LAST UPDATED: 23 JUL 2003 <20030723/UP>
MOST RECENT DERWENT UPDATE: 200347 <200347/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> NEW WEEKLY SDI FREQUENCY AVAILABLE --> see NEWS <<<

>>> SLART (Simultaneous Left and Right Truncation) is now available in the /ABEX field. An additional search field /BIX is also provided which comprises both /BI and /ABEX <<<

>>> PATENT IMAGES AVAILABLE FOR PRINT AND DISPLAY <<<

>>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES, SEE <http://www.derwent.com/dwpi/updates/dwpicov/index.html> <<<

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE, PLEASE VISIT:
http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<

>>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER GUIDES, PLEASE VISIT:

http://www.derwent.com/userguides/dwpi_guide.html <<<

=> d que 133

L24	3123	SEA FILE=WPIX ABB=ON	PLU=ON	?CAROTEN?	
L25	40704	SEA FILE=WPIX ABB=ON	PLU=ON	?FERMENT?	
L26	1546	SEA FILE=WPIX ABB=ON	PLU=ON	CULTUR? MEDIA	
L27	37669	SEA FILE=WPIX ABB=ON	PLU=ON	MICROB?	
L28	236	SEA FILE=WPIX ABB=ON	PLU=ON	L24 AND (L25 OR L26 OR L27)	
L29	15	SEA FILE=WPIX ABB=ON	PLU=ON	L28 AND OXYGEN	
L30	1	SEA FILE=WPIX ABB=ON	PLU=ON	L28 AND O2	
L31	16	SEA FILE=WPIX ABB=ON	PLU=ON	(L29 OR L30)	
L32	11	SEA FILE=WPIX ABB=ON	PLU=ON	L31 NOT (SKIN OR DOUGH OR EMBDEN-MEYERHOF)/TI	
L33	4	SEA FILE=WPIX ABB=ON	PLU=ON	L32 AND (CANTHAXANTHIN OR CHEMICALLY DEFINED OR NUTRIENT OR CONCENTRATES)/TI	4 cites

=> d que 140

L24	3123	SEA FILE=WPIX ABB=ON	PLU=ON	?CAROTEN?	
L25	40704	SEA FILE=WPIX ABB=ON	PLU=ON	?FERMENT?	
L26	1546	SEA FILE=WPIX ABB=ON	PLU=ON	CULTUR? MEDIA	
L27	37669	SEA FILE=WPIX ABB=ON	PLU=ON	MICROB?	
L28	236	SEA FILE=WPIX ABB=ON	PLU=ON	L24 AND (L25 OR L26 OR L27)	
L29	15	SEA FILE=WPIX ABB=ON	PLU=ON	L28 AND OXYGEN	
L30	1	SEA FILE=WPIX ABB=ON	PLU=ON	L28 AND O2	
L31	16	SEA FILE=WPIX ABB=ON	PLU=ON	(L29 OR L30)	
L36	685	SEA FILE=WPIX ABB=ON	PLU=ON	L24(5A)(PRODUC? OR PREP?)	
L37	46	SEA FILE=WPIX ABB=ON	PLU=ON	L36 AND OXYGEN?	
L38	19	SEA FILE=WPIX ABB=ON	PLU=ON	L37 AND (MICROB? OR L25 OR CULTUR?)	
L39	11	SEA FILE=WPIX ABB=ON	PLU=ON	L38 NOT L31	
L40	1	SEA FILE=WPIX ABB=ON	PLU=ON	L39 AND STIRRING/TI	1 cite

=> s 133 or 140

L80 5 L33 OR L40 5 cites total for WPIX

=> dup rem 149 167 158 179 180 removing duplicate citations
FILE 'MEDLINE' ENTERED AT 12:08:32 ON 28 JUL 2003

FILE 'CABA' ENTERED AT 12:08:32 ON 28 JUL 2003
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FILE 'WPIX' ENTERED AT 12:08:32 ON 28 JUL 2003
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PROCESSING COMPLETED FOR L49
PROCESSING COMPLETED FOR L67
PROCESSING COMPLETED FOR L58
PROCESSING COMPLETED FOR L79

PROCESSING COMPLETED FOR L80

L81 17 DUP REM L49 L67 L58 L79 L80 (2 DUPLICATES REMOVED) *17 cites total*
 ANSWERS '1-2' FROM FILE MEDLINE
 ANSWER '3' FROM FILE CABA
 ANSWERS '4-6' FROM FILE BIOTECHNO
 ANSWERS '7-12' FROM FILE HCAPLUS
 ANSWERS '13-17' FROM FILE WPIX

=> d ibib abs ind 1-2 *indexing*

L81 ANSWER 1 OF 17 MEDLINE on STN
 ACCESSION NUMBER: 74298770 MEDLINE
 DOCUMENT NUMBER: 74298770 PubMed ID: 4850775
 TITLE: **Biogenesis** of beta-carotene in *Mycobacterium*
kansasii.
 AUTHOR: David H L
 SOURCE: JOURNAL OF BACTERIOLOGY, (1974 Aug) 119 (2) 527-33.
 Journal code: 2985120R. ISSN: 0021-9193.
 Report No.: NASA-74298770.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals; Space Life Sciences
 ENTRY MONTH: 197410
 ENTRY DATE: Entered STN: 19900310
 Last Updated on STN: 19900310
 Entered Medline: 19741025

CT Acetates: ME, metabolism
 Amines: PD, pharmacology
 Biogenesis
 Carbon Radioisotopes
 *Carotenoids: BI, biosynthesis
 Chloramphenicol: PD, pharmacology
 Chromatography, Thin Layer
 Darkness
 Light
 *Mycobacterium: ME, metabolism
 Oxygen
 RNA, Bacterial: BI, biosynthesis
 Rifampin: PD, pharmacology
 Spectrophotometry
 Temperature
 Time Factors
 Tritium
 Uracil: ME, metabolism

*no abstract given
 for 1st 2 citations*

RN 10028-17-8 (Tritium); 13292-46-1 (Rifampin); 36-88-4 (Carotenoids);
 56-75-7 (Chloramphenicol); 66-22-8 (Uracil); 7782-44-7 (Oxygen)
 CN 0 (Acetates); 0 (Amines); 0 (Carbon Radioisotopes); 0 (RNA, Bacterial)

L81 ANSWER 2 OF 17 MEDLINE on STN
 ACCESSION NUMBER: 73227417 MEDLINE
 DOCUMENT NUMBER: 73227417 PubMed ID: 4665108
 TITLE: Studies on natural photo-protectors. II. The influence of
 oxygen and temperature on photosensitivity of mutants of
Aspergillus giganteus with various ability of
 carotenoid synthesis.
 AUTHOR: Lazarski R
 SOURCE: FOLIA BIOLOGICA, (1972) 20 (3) 279-86.
 Journal code: 2984758R. ISSN: 0015-5497.
 PUB. COUNTRY: Poland

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 197310
 ENTRY DATE: Entered STN: 19900310
 Last Updated on STN: 19900310
 Entered Medline: 19731005

CT Aerobiosis
 Anaerobiosis
 *Aspergillus: ME, metabolism
 *Carotenoids: BI, biosynthesis
 Genetics, Microbial
 *Light
 Mutation
 *Oxygen
 *Temperature
 RN 36-88-4 (Carotenoids); 7782-44-7 (Oxygen)

=> d ibib abs ind 3

L81 ANSWER 3 OF 17 CABA COPYRIGHT 2003 CABI on STN

ACCESSION NUMBER: 83:112346 CABA
 DOCUMENT NUMBER: 831980736
 TITLE: The role of oxygen concentration in the synthesis of
 carotenoids, poly- beta -hydroxybutyrate and
 succinate oxidase in continuous
 culture of Azospirillum
 AUTHOR: Nur, I.; Okon, Y.; Henis, Y.
 CORPORATE SOURCE: Dep. of Plant Path. and Microbiology, Hebrew Univ.
 of Jerusalem, P.O. Box 12, Rehovot 76100, Israel.
 SOURCE: Israel Journal of Botany, (1982) Vol. 31, No. 1-4,
 pp. 221-227. 19 ref.
 ISSN: 0021-213X
 DOCUMENT TYPE: Conference Article; Journal
 LANGUAGE: English

AB Azospirillum brasilense strain Cd was grown in ammonium-malate-mineral
 salts medium under various dissolved oxygen tensions. Maximum poly- beta
 -hydroxybutyrate content was observed under microaerobic conditions and
 intermediate dilution rates. Highest cell yield and respiration rate were
 obtained at relatively low oxygen. Protein content was higher at high
 oxygen levels. Succinate oxidase and succinate
 dehydrogenase activities were especially high under high oxygen. Four
 carotenoids were isolated and purified from membranes. In the
 presence of diphenylamine which inhibits carotenoid synthesis,
 the rate of acetylene reduction decreased to 50% of the control. In liquid
 cultures, carotenoid synthesis was initiated only after
 the depletion of NH₄Cl when N₂ fixing activity became evident.
 Carotenoids appeared to protect nitrogenase from oxidative damage.
 CC EE110 Agricultural Economics; DD500 Laws and Regulations; DD100
 Administration of Agencies and Organizations; CC200 Extension and Advisory
 Work; UU000 Sociology (General); JJ100 Soil Biology
 BT prokaryotes; Azospirillum; Spirillaceae; Gracilicutes; bacteria
 CT Nitrogen Fixation; enzymes; oxygen
 ST specific taxa
 RN 7782-44-7
 ORGN bacteria; Azospirillum brasilense

=> d ibib abs ind 4-6

L81 ANSWER 4 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN
DUPLICATE

ACCESSION NUMBER: 1999:30021700 BIOTECHNO
TITLE: **Control** of both **foam** and dissolved **oxygen** in the presence of a surfactant for production of **.beta.-carotene** in *Blakeslea trispora*
AUTHOR: Seon-Won K.; Lee I.-Y.; Jeong J.-C.; Lee J.-H.; Park Y.-H.
CORPORATE SOURCE: I.-Y. Lee, Bioprocess Technol. Res. Division, Korea Res. Inst. of Biosci./Biotech., P.O. Box 115, Yusong, Taejon 305-600, South Korea.
E-mail: leeiy@mail.kribb.re.kr
SOURCE: Journal of Microbiology and Biotechnology, (1999), 9/5 (548-553), 20 reference(s)
CODEN: JOMBES ISSN: 1017-7825
DOCUMENT TYPE: Journal; Article
COUNTRY: Korea, Republic of
LANGUAGE: English
SUMMARY LANGUAGE: English

AN 1999:30021700 BIOTECHNO

AB A production of **.beta.-carotene** was attempted in a fed-batch **culture** of *Blakeslea trispora* by **controlling** both foam and dissolved **oxygen** in the presence of surfactant, Span 20. Results obtained from the shake flask **cultures** indicated that a high **concentration** of dissolved **oxygen** was needed for both cell growth and **.beta.-carotene** synthesis, and the optimal concentration of glucose was found to be in the range of 50-100 g/l. In order to maintain the dissolved **oxygen concentration** level at higher than 50% of air saturation, pure **oxygen** was automatically sparged into the medium with air. Foam was controlled by bypassing air from the submerged **aeration** to the headspace in response to the foam that was caused by Span 20. High agitation speed was found to be detrimental to the cell growth due to shear damage, even though it provided sufficient dissolved **oxygen**. On the other hand, a low **aeration** speed caused stagnant regions in the **fermentor** because of improper mixing. Thus, for the fed-batch operation, agitation speed was increased gradually from 300 to 700 rpm to prevent cell damage at the initial stage of **fermentation** and to give efficient mixing for a viscous **culture** broth as the **culture** proceeded. By **controlling** dissolved **oxygen** and foam, a high **concentration** of **.beta.-carotene** (1,190 mg/l) was obtained in 6 days of the fed-batch **culture** of *B. trispora* with 2.5% of the dry cell weight, which was approximately 5 times higher than that of the batch **cultures**.

CT *dissolved **oxygen**; *surfactant; *sorbitan laurate; *beta **carotene**; *biotechnology; *protein synthesis; * **fermentation**; *fungus; *blakeslea trispora; glucose; foam; **oxygen concentration**; shear stress; bioreactor; fungus mutant; light exposure; oxidative stress; centrifugation; high performance liquid chromatography; mycelium; cell growth; nonhuman; article

RN (sorbitan laurate) 1338-39-2; (beta **carotene**) 7235-40-7; (glucose) 50-99-7, 84778-64-3

L81 ANSWER 5 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN
DUPLICATE

ACCESSION NUMBER: 1997:27485777 BIOTECHNO

TITLE: Influence of **oxygen** and glucose on primary metabolism and astaxanthin production by *Phaffia rhodozyma* in batch and fed-batch **cultures**: Kinetic and **stoichiometric** analysis

AUTHOR: Yamane Y.-I.; Higashida K.; Nakashimada Y.; Kakizono T.; Nishio N.

CORPORATE SOURCE: N. Nishio, Fermentation Technology Department, Faculty of Engineering, Hiroshima University, Kagamiyama 1-4-1, Higashi-Hiroshima 739, Japan.
E-mail: nnishio@ipc.hiroshima-u.ac.jp

SOURCE: Applied and Environmental Microbiology, (1997), 63/11 (4471-4478), 35 reference(s)
CODEN: AEMIDF ISSN: 0099-2240

DOCUMENT TYPE: Journal; Article

COUNTRY: United States

LANGUAGE: English

SUMMARY LANGUAGE: English

AN 1997:27485777 BIOTECHNO

AB The influence of the **oxygen** and glucose supply on primary metabolism (**fermentation**, respiration, and anabolism) and astaxanthin production in the yeast *Phaffia rhodozyma* was investigated. When *P. rhodozyma* grew under **fermentative** conditions with limited **oxygen** or high **concentrations** of glucose, the astaxanthin production rate decreased remarkably. On the other hand, when the yeast grew under **aerobic** conditions, the astaxanthin production rate increased with increasing **oxygen** uptake. A kinetic analysis showed that the respiration rate correlated positively with the astaxanthin production rate, whereas there was a negative correlation with the ethanol production rate. The influence of glucose concentration at a fixed nitrogen **concentration** with a high level of **oxygen** was then investigated. The results showed that astaxanthin production was enhanced by an initial high carbon/nitrogen ratio (C/N ratio) present in the medium, but cell growth was inhibited by a high glucose concentration. A stoichiometric analysis suggested that astaxanthin production was enhanced by decreasing the amount of NADPH required for anabolism, which could be achieved by the repression of protein biosynthesis with a high C/N ratio. Based on these results, we performed a two-stage fed-batch **culture**, in which cell growth was enhanced by a low C/N ratio in the first stage and astaxanthin production was enhanced by a high C/N ratio in the second stage. In this **culture** system, the highest astaxanthin production, 16.0 mg per liter, was obtained.

CT *astaxanthin; *phaffia rhodozyma; *yeast; carbon; **carotenoid**; glucose; nitrogen; **oxygen**; reduced nicotinamide adenine dinucleotide phosphate; article; **culture** medium; fungus **culture**; fungus growth; kinetics; nonhuman; stoichiometry

RN (astaxanthin) 472-61-7; (carbon) 7440-44-0; (glucose) 50-99-7, 84778-64-3; (nitrogen) 7727-37-9; (**oxygen**) 7782-44-7; (reduced nicotinamide adenine dinucleotide phosphate) 53-57-6

L81 ANSWER 6 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN

ACCESSION NUMBER: 1999:29160364 BIOTECHNO

TITLE: Effect of **culture** condition on the biosynthesis of **carotenoids** in *Rhodotorula glutinis* No. 21

AUTHOR: Sakaki H.; Nochide H.; Nakanishi T.; Miki W.; Fujita T.; Komemushi S.

CORPORATE SOURCE: H. Sakaki, Department of Agricultural Chemistry, Faculty of Agriculture, Kinki University, 3327-204 Nakamachi, Nara 631-8505, Japan.

SOURCE: Seibutsu-kogaku Kaishi, (1999), 77/2 (55-59), 13
reference(s)
CODEN: SEKAEA ISSN: 0919-3758

DOCUMENT TYPE: Journal; Article
COUNTRY: Japan
LANGUAGE: Japanese
SUMMARY LANGUAGE: English; Japanese

AN 1999:29160364 BIOTECHNO

AB Changes in the biosynthesis of **carotenoids** caused by altering the **culture** conditions of the yeast *Rhodotorula glutinis* No. 21 were investigated. Cells grown on lactate showed a higher production of torularhodin, one of the final products, compared with those grown on glucose, but no changes were observed as a result of adjusting the pH, at the start of the cultivation. These findings suggested that the difference in the carbon source was a factor giving rise to a change in the **carotenoid** biosynthesis system of *R. glutinis* No. 21. Increases in the contents of torulene and torularhodin were related to elevation of the dissolved **oxygen concentration**, which was adjusted by **aeration**. It was concluded that this yeast switches its system of **carotenoid** biosynthesis according to the extracellular conditions. The results obtained will contribute to elucidating the role of torularhodin in this non-phototrophic yeast which produces two **carotenoids**, **.beta.-carotene** and torularhodin, as the final products.

CT *biosynthesis; ***carotenoid**; *Rhodotorula glutinis*; lactic acid; torularhodin; glucose; pH; torulene; dissolved **oxygen**; **aeration**; **beta carotene**

=> d ibib abs hitrn ind 7-12

L81 ANSWER 7 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2003:320046 HCAPLUS
DOCUMENT NUMBER: 138:302755
TITLE: Microorganism and production of carotenoid compounds thereby

INVENTOR(S): Yamaoka, Yukiho
PATENT ASSIGNEE(S): National Institute of Advanced Industrial Science and Technology, Japan

SOURCE: PCT Int. Appl., 24 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003033683	A1	20030424	WO 2002-JP10619	20021011
W: CN, US				
RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR				
JP 2003189846	A2	20030708	JP 2002-231126	20020808
PRIORITY APPLN. INFO.:				
			JP 2001-318746	A 20011016
			JP 2002-132190	A 20020507
			JP 2002-231126	A 20020808

AB Astaxanthin and canthaxanthin are manufd. com. with marine *Thraustochytrium* sp. CHN-3 (FERM P-18556) of *Labyrinthula* by aerobic fermn. under illumination. The astaxanthin and canthaxanthin are isolated from the microorganism by solvent extn. and chromatog.

- IT 7782-44-7, Oxygen, biological studies
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IC ICM C12N001-14
 ICS C12P023-00; C12R001-645
- CC 16-2 (Fermentation and Bioindustrial Chemistry)
 Section cross-reference(s): 1, 17, 63
- ST astaxanthin canthaxanthin manuf Thraustochytrium Labyrinthula culture
 medium
- IT **Fermentation**
 (aerobic; astaxanthin and canthaxanthin manuf. with marine
 Thraustochytrium)
- IT Carbon sources, microbial
Culture media
 Feed
 Health food
 Illumination
 Labyrinthula
 Nitrogen sources, microbial
 Seawater
 Solvent extraction
 Thraustochytrium
 pH
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IT **Carotenes, preparation**
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
 (Preparation)
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IT Vitamins
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IT Light
 (blue; astaxanthin and canthaxanthin manuf. with marine
 Thraustochytrium)
- IT Light
 (red; astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IT 50-99-7, D-Glucose, biological studies 57-13-6, Urea, biological studies
 57-48-7, D-Fructose, biological studies 57-50-1, Sucrose, biological
 studies 59-43-8, Thiamine, biological studies 67-56-1, Methyl alcohol,
 biological studies 67-64-1, Acetone, biological studies 67-66-3,
 Chloroform, biological studies 7664-41-7, Ammonia, biological studies
 7757-79-1, Potassium nitrate, biological studies 7782-44-7,
 Oxygen, biological studies
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS
 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 8 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:181867 HCAPLUS

DOCUMENT NUMBER: 138:236950

TITLE: Effect of the aeration rate and agitation speed on
 .beta.-carotene production and morphology of *Blakeslea*
trisporea in a stirred tank reactor: mathematical
 modeling

AUTHOR(S): Mantzouridou, F.; Roukas, T.; Kotzekidou, P.
 CORPORATE SOURCE: Department of Food Science and Technology, Aristotle

University of Thessaloniki, Thessaloniki, 54006,
Greece
SOURCE: Biochemical Engineering Journal (2002), 10(2), 123-135
CODEN: BEJOFV; ISSN: 1369-703X
PUBLISHER: Elsevier Science S.A.
DOCUMENT TYPE: Journal
LANGUAGE: English

- AB The effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in a stirred tank reactor was investigated. *B. trispora* formed hyphae, zygothores and zygosporos during the fermn. The zygosporos were the morphol. form responsible for .beta.-carotene prodn. Both aeration and agitation significantly affected .beta.-carotene concn., productivity, biomass and the volumetric mass transfer coeff. (KLa). The highest .beta.-carotene concn. (1.5 kg m⁻³) and the highest productivity (0.08 kg m⁻³ per day) were obtained at low impeller speed (150 rpm) and high aeration rate (1.5 vvm). Also, max. productivity (0.08 kg m⁻³ per day) and biomass dry wt. (26.4 kg m⁻³) were achieved at high agitation speed (500 rpm) and moderate aeration rate (1.0 vvm). Conversely, the highest value of KLa (0.33 s⁻¹) was obsd. at high agitation speed (500 rpm) and high aeration rate (1.5 vvm). The expts. were arranged according to a central composite statistical design. Response surface methodol. was used to describe the effect of impeller speed and aeration rate on the most important fermn. parameters. In all cases, the fit of the model was found to be good. All fermn. parameters (except biomass concn.) were strongly affected by the interactions among the operation variables. .beta.-Carotene concn. and productivity were significantly influenced by the aeration, agitation, and by the pos. or neg. quadratic effect of the aeration rate. Biomass concn. was principally related to the aeration rate, agitation speed, and the pos. or neg. quadratic effect of the impeller speed and aeration rate, resp. Finally, the volumetric mass transfer coeff. was characterized by the significant effect of the agitation speed, while the aeration rate had a small effect on KLa.
- IT 7782-44-7, Oxygen, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(dissolved; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in stirred tank reactor)
- IT 7235-40-7P, .beta.-Carotene
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in stirred tank reactor)
- CC 16-2 (Fermentation and Bioindustrial Chemistry)
- ST *Blakeslea beta carotene* fermn aeration agitation model
- IT Fermentation
(batch; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in stirred tank reactor)
- IT Mass transfer
(gas-liq., KLa; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in stirred tank reactor)
- IT Aeration
Agitation (mechanical)
Blakeslea trispora
Cell morphology
Simulation and Modeling, biological
(modeling of the effect of aeration rate and agitation speed on

- .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)
- IT Optimization
(statistical; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)
- IT Fermentation apparatus
(stirred-tank fermentor; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)
- IT 7782-44-7, Oxygen, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(dissolved; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)
- IT 7235-40-7P, .beta.-Carotene
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 9 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:924027 HCAPLUS
DOCUMENT NUMBER: 136:52783
TITLE: Process for producing carotenoid pigments
INVENTOR(S): Tsubokura, Akira; Mizuta, Haruyoshi
PATENT ASSIGNEE(S): Nippon Mitsubishi Oil Corporation, Japan
SOURCE: PCT Int. Appl., 23 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001096591	A1	20011220	WO 2001-JP4874	20010608
W: AU, CA, CN, IL, KR, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
JP 2001352995	A2	20011225	JP 2000-175124	20000612
AU 2001062730	A5	20011224	AU 2001-62730	20010608
EP 1229126	A1	20020807	EP 2001-936932	20010608
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
US 2003044886	A1	20030306	US 2002-49228	20020211
PRIORITY APPLN. INFO.:			JP 2000-175124	A 20000612
			WO 2001-JP4874	W 20010608

- AB A process for the microbial manuf. of carotenoids of desired ratio of carotenoid compds. with bacteria E-396 and A-581-1 which have low growth rate and enable easy isolation of the carotenoids was given. The ratio of the carotenoid compds. (i.e., astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin, zeaxanthin, .beta.-cryptoxanthin, 3-hydroxyechinenone, adonirubin, etc.) is controlled by the concn. of oxygen dissolved in a liq. culture medium during the fermn.
- IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin

514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone

4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin

7235-40-7P, .beta.-Carotene

RL: BPN (Biosynthetic preparation); BIOL (Biological study); **PREP (Preparation)**

(process for producing carotenoid pigments)

IT 7782-44-7, Oxygen, biological studies

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(process for producing carotenoid pigments)

IC ICM C12P023-00

CC 16-2 (Fermentation and Bioindustrial Chemistry)

ST carotenoid manuf bacteria dissolved oxygen

IT rRNA

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(16 S, gene for; process for producing carotenoid pigments)

IT Bacteria (Eubacteria)

Culture media

DNA sequences

Fermentation

Taxonomy

(process for producing carotenoid pigments)

IT **Carotenes, preparation**

RL: BPN (Biosynthetic preparation); BIOL (Biological study); **PREP**

(Preparation)

(process for producing carotenoid pigments)

IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)

(process for producing carotenoid pigments)

IT 382660-64-2 382660-65-3

RL: PRP (Properties)

(nucleotide sequence; process for producing carotenoid pigments)

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone

472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin

514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone

4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin

7235-40-7P, .beta.-Carotene

RL: BPN (Biosynthetic preparation); BIOL (Biological study); **PREP**

(Preparation)

(process for producing carotenoid pigments)

IT 7782-44-7, Oxygen, biological studies

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(process for producing carotenoid pigments)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 10 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:691371 HCAPLUS

DOCUMENT NUMBER: 135:370671

TITLE: Application of a complete factorial design for the
production of zeaxanthin by Flavobacterium sp.

AUTHOR(S): Masetto, Alejandra; Flores-Cotera, Luis B.; Diaz,
Carlos; Langley, Elizabeth; Sanchez, Sergio

CORPORATE SOURCE: Departamento de Biologia Molecular y Biotecnologia del
Instituto de Investigaciones Biomedicas, Universidad
Nacional Autonoma de Mexico, Mexico, 04510, Mex.

SOURCE: Journal of Bioscience and Bioengineering (2001),
92(1), 55-58

CODEN: JBBIF6; ISSN: 1389-1723

PUBLISHER: Society for Bioscience and Bioengineering, Japan

DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Utilizing a four-liter fermentor and applying a complete factorial design 23, the combined effects of agitation speed, aeration rate, and corn steep liquor concn. on zeaxanthin prodn. by *Flavobacterium* sp. were studied. Maximum growth and prodn. of total carotenoids and zeaxanthin were obtained at 600 rpm, 2 vvm and 4.6% corn steep liquor. Under these conditions, zeaxanthin represented 86% of the total carotenoids produced. Lower values of the variables studied resulted in lower growth, volumetric prodn. of zeaxanthin and total carotenoids, and favored the formation of other carotenoids such as .beta.-carotene and canthaxanthin. The pos. effects on growth and total carotenoids and zeaxanthin formation were in a large extent due to the interaction of agitation/corn steep liquor. However, aeration also had a pos. effect on growth.

IT 144-68-3P, Zeaxanthin 514-78-3P, Canthaxanthin

7235-40-7P, .beta.-Carotene

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP

(Preparation)

(application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT 7782-44-7, Oxygen, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dissolved; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

CC 16-2 (Fermentation and Bioindustrial Chemistry)

ST *Flavobacterium* zeaxanthin fermn optimization

IT Fermentation

(aerobic; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT Aeration

Agitation (mechanical)

Flavobacterium

Growth, microbial

(application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT Carotenes, preparation

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP

(Preparation)

(application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT Industrial liquors

(corn steep liquor; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT Optimization

(statistical; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT 144-68-3P, Zeaxanthin 514-78-3P, Canthaxanthin

7235-40-7P, .beta.-Carotene

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP

(Preparation)

(application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT 7782-44-7, Oxygen, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dissolved; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

REFERENCE COUNT:

15

THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 2002:118119 HCAPLUS
 DOCUMENT NUMBER: 136:133689
 TITLE: Production of .beta.-carotene from Blakeslea trispora
 INVENTOR(S): Park, Yeong Hoon; Lee, In Yeong; Kim, Seon Won; Lee, Jung Heon; Jeong, Jae Cheol
 PATENT ASSIGNEE(S): Korea Institute of Science and Technology, S. Korea
 SOURCE: Repub. Korean Kongkae Taeho Kongbo, No pp. given
 CODEN: KRXXA7
 DOCUMENT TYPE: Patent
 LANGUAGE: Korean
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
KR 2000031738	A	20000605	KR 1998-47930	19981110
PRIORITY APPLN. INFO.:			KR 1998-47930	19981110

AB Addn. of a surfactant in the medium to increase the prodn. of .beta.-carotene by a Blakeslea trispora culture causes foaming during fermn. An anti-foaming agent can be used to control foam, but it inhibits the growth of the fungi. Submerged aeration accompanied with surface aeration and control of stirring speed can be used effectively to control foam and increase the yield of .beta.-carotene from Blakeslea. In the fermn. process, the anti-foam agent, Span 20 is used to control foam. In addn. to anti-foam agent, submerged and surface aeration are applied to control foam. The total aeration rate is controlled in the range of 0.5-3.0 L air/L medium/min depending on the growth state of fungi. The speed of stirring is increased stepwise in the range of 10-100 rpm reached at 150-800 rpm depending on the increase of cell mass. The main source of carbon is glucose and the optimal concn. is kept under 70 g/L supplied intermittently. Pure oxygen is supplied to increase the dissolved oxygen in the medium. The final yield of .beta.-carotene is 17 g/L.

IT 7235-40-7P, .beta.-Carotene
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
 (prodn. of .beta.-carotene from Blakeslea trispora)

IC ICM C12P023-00
 CC 16-2 (Fermentation and Bioindustrial Chemistry)
 ST Blakeslea beta carotene fermn foam control
 IT Fermentation
 (fed-batch; prodn. of .beta.-carotene from Blakeslea trispora)

IT Aeration
 Agitation (mechanical)
 Blakeslea trispora
 Foaming
 (prodn. of .beta.-carotene from Blakeslea trispora)

IT 7235-40-7P, .beta.-Carotene
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
 (prodn. of .beta.-carotene from Blakeslea trispora)

IT 1338-39-2, Span 20
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (prodn. of .beta.-carotene from Blakeslea trispora)

L81 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1994:215496 HCAPLUS
 DOCUMENT NUMBER: 120:215496

TITLE: Fermentative manufacture of .beta.-carotene.
 INVENTOR(S): Matsumura, Shigeo; Sumino, Yasuhiro; Matsui, Junji
 PATENT ASSIGNEE(S): Takeda Chemical Industries, Ltd., Japan
 SOURCE: Eur. Pat. Appl., 12 pp.
 CODEN: EPXXDW
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 586255	A1	19940309	EP 1993-306964	19930902
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, PT, SE				
CA 2105527	AA	19940304	CA 1993-2105527	19930903
JP 06153986	A2	19940603	JP 1993-219427	19930903
PRIORITY APPLN. INFO.:			JP 1992-236176	19920903

AB .beta.-Carotene is manufd. using a microalga tolerant to an active O generator, such as methylene blue and rose bengal, and capable of producing .beta.-carotene. The microalga is preferably Chlorella pyrenoidosa.
 IT 7235-40-7P, .beta.-Carotene
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
 (manuf. of, fermentative, with Chlorella pyrenoidosa)
 IT 7782-44-7, Oxygen, biological studies
 RL: BIOL (Biological study)
 (singlet, in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa)
 IC ICM C12P023-00
 ICS C12N001-12
 ICI C12P023-00, C12R001-89
 CC 16-8 (Fermentation and Bioindustrial Chemistry)
 ST fermn Chlorella beta carotene
 IT Chlorella pyrenoidosa
 (.beta.-carotene manuf. by fermn. with)
 IT Fermentation
 (.beta.-carotene, with Chlorella pyrenoidosa)
 IT 61-73-4, Methylene blue 11121-48-5, Rose bengal
 RL: BIOL (Biological study)
 (in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa)
 IT 7235-40-7P, .beta.-Carotene
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
 (manuf. of, fermentative, with Chlorella pyrenoidosa)
 IT 7782-44-7, Oxygen, biological studies
 RL: BIOL (Biological study)
 (singlet, in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa)

=> d ibib abs 13-17

L81 ANSWER 13 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN
 ACCESSION NUMBER: 1998-467550 [40] WPIX
 DOC. NO. CPI: C1998-141821
 TITLE: Fermentative production of valuable compound(s)
 - by fermentation of a microbial strain on an industrial scale using a chemically defined medium and recovery of the compound(s).

DERWENT CLASS: B04 D16
 INVENTOR(S): DE LAAT, W T A; KOEKMAN, B P; PREUSTING, J C G; DE LAAT, W T A M
 PATENT ASSIGNEE(S): (KONN) GIST-BRÖCADES BV; (STAM) DSM NV; (DLAA-I) DE LAAT W T A M; (KOEK-I) KOEKMAN B P; (PREU-I) PREUSTING J C G
 COUNTRY COUNT: 82
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9837179	A2	19980827	(199840)*	EN	37
RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW					
AU 9864000	A	19980909	(199905)		
EP 970236	A2	20000112	(200008)	EN	
R: AL AT BE CH DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
CZ 9902954	A3	20000412	(200026)		
BR 9807362	A	20000418	(200032)		
CN 1248294	A	20000322	(200032)		
KR 2000075487	A	20001215	(200131)		
MX 9907691	A1	20000601	(200133)		
JP 2001512970	W	20010828	(200156)		44
US 2002039758	A1	20020404	(200227)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9837179	A2	WO 1998-EP1122	19980220
AU 9864000	A	AU 1998-64000	19980220
EP 970236	A2	EP 1998-909483	19980220
		WO 1998-EP1122	19980220
CZ 9902954	A3	WO 1998-EP1122	19980220
		CZ 1999-2954	19980220
BR 9807362	A	BR 1998-7362	19980220
		WO 1998-EP1122	19980220
CN 1248294	A	CN 1998-802632	19980220
KR 2000075487	A	WO 1998-EP1122	19980220
		KR 1999-707546	19990819
MX 9907691	A1	MX 1999-7691	19990819
JP 2001512970	W	JP 1998-536284	19980220
		WO 1998-EP1122	19980220
US 2002039758	A1 Div ex	US 1999-367029	19991025
		US 2001-982474	20011017

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9864000	A Based on	WO 9837179
EP 970236	A2 Based on	WO 9837179
CZ 9902954	A3 Based on	WO 9837179
BR 9807362	A Based on	WO 9837179
KR 2000075487	A Based on	WO 9837179
JP 2001512970	W Based on	WO 9837179

PRIORITY APPLN. INFO: EP 1997-200494 19970220

AN 1998-467550 [40] WPIX

AB WO 9837179 A UPAB: 19981008

A process for the production of a valuable compound comprises: (a) **fermentation** of a **microbial** strain of an industrial scale in a **fermentation** medium which is a chemically defined medium composed of chemically defined constituents; and (b) recovery of the valuable compound from the **fermentation** broth.

Also claimed is a method for preparing and/or improving a **microbial** strain producing a valuable compound of interest which is capable of being **fermented** on an industrial scale in a chemically defined medium, comprising: (a) subjecting a suitable parent strain to a mutagenic treatment selected from physical mutagens and chemical mutagens, and/or to DNA transformation; (b) screening the resulting mutants and/or transformants for their growth performance on a chemically defined medium and their production level of the valuable compound of interest; (c) selecting mutants and/or transformants which have a good growth performance on a chemically defined medium and/or an improved production level of the valuable compound of interest as compared to the parent strain.

USE - The method can be used for the production of valuable compounds such as beta-lactam compounds, enzymes, astaxanthin, arachidonic acid, triglycerides, beta-**carotene**, glucose isomerase (GI), clavulanic acid or erythromycin (claimed).

ADVANTAGE - The productivity of **microbial** strains in chemically defined media, when measured on an industrial scale, may be comparable to or in some cases even higher than their productivity in complex media. **Oxygen** transfer from the gas phase to the liquid phase and the carbon dioxide transfer from the liquid phase to the gas phase is improved substantially as compared to using complex media. The use of chemically defined media has a favourable influence on morphology, i.e. by producing a more rigid pellet which does not easily fall apart during **fermentation**. In addition, the chemically defined medium can decrease the viscosity of filamentous **fermentation** broths and improve downstream processing.

Dwg.0/2

L81 ANSWER 14 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 1995-053688 [08] WPIX

DOC. NO. CPI: C1995-024479

TITLE: New bacteria which produce **carotenoid** pigments
- used for the prodn. of astaxanthin, adonixanthin, beta-**carotene**, echinenone, **canthaxanthin** and zeaxanthin.

DERWENT CLASS: B04 B05 D13 D16 D21 E24

INVENTOR(S): KIYOTA, T; TAKAKI, M; TSUBOKURA, A; YONEDA, H

PATENT ASSIGNEE(S): (NIOC) NIPPON OIL KK; (MISQ) NIPPON MITSUBISHI OIL CORP;
(NIOC) NIPPON OIL CO LTD; (NIOC) NIPPON MITSUBISHI OIL CORP

COUNTRY COUNT: 9

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 635576	A1	19950125	(199508)*	EN	29
R: CH DE FR GB LI					
NO 9402731	A	19950123	(199511)		
CA 2128549	A	19950123	(199516)		
JP 07079796	A	19950328	(199521)		20

US 5607839 A 19970304 (199715) 16
 US 5858761 A 19990112 (199910)
 EP 635576 B1 20000830 (200042) EN
 R: CH DE FR GB LI
 DE 69425706 E 20001005 (200057)
 JP 3242531 B2 20011225 (200203) 20
 NO 313204 B1 20020826 (200263)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 635576	A1	EP 1994-111525	19940722
NO 9402731	A	NO 1994-2731	19940721
CA 2128549	A	CA 1994-2128549	19940721
JP 07079796	A	JP 1994-152240	19940704
US 5607839	A	US 1994-276943	19940719
US 5858761	A Div ex	US 1994-276943	19940719
		US 1996-716841	19960919
EP 635576	B1	EP 1994-111525	19940722
DE 69425706	E	DE 1994-625706	19940722
		EP 1994-111525	19940722
JP 3242531	B2	JP 1994-152240	19940704
NO 313204	B1	NO 1994-2731	19940721

FILING DETAILS:

PATENT NO	KIND	PATENT NO
US 5858761	A Div ex	US 5607839
DE 69425706	E Based on	EP 635576
JP 3242531	B2 Previous Publ.	JP 07079796
NO 313204	B1 Previous Publ.	NO 9402731

PRIORITY APPLN. INFO: JP 1993-181615 19930722

AN 1995-053688 [08] WPIX

AB EP 635576 A UPAB: 19950301

Bacteria belonging to a new genus and having the following properties are claimed: (1) morphology: polymorphic rod; (2) motility: motile; (3) flagella: peritrichous; (4) spore formation: none; (5) gram strain: negative; (6) prodn. of pigment: positive (water insoluble); (7) oxidase: positive; (8) catalase: positive; (9) behaviour toward oxygen: aerobic; (10) fermentation of glucose: negative; (11) prodn. of 3-ketolactose: negative; (12) quinone type: Q-10; (13) GC content of intracellular DNA: 64-69 molar %; (14) formation of slime: glucose, negative; sucrose, negative; (15) presence of sphingolipid: negative; (16) presence of bacteriochlorophyll: negative.

USE - The bacteria can be cultured to produce one or a mixt. of **carotenoid** pigments selected from astaxanthin, adonixanthin, beta-carotene, echinenone, canthaxanthin and zeaxanthin. The **carotenoid** pigments can be used as additives in food, feed, pharmaceuticals, cosmetics, etc.

ADVANTAGE - Using the bacteria, **carotenoids** can be produced on an industrial scale. They can produce natural type astaxanthin., Almost 100% of astaxanthin produced by the bacteria is (3S,3'S)-astaxanthin.
 Dwg.0/6

ABEQ US 5607839 A UPAB: 19970410

A new process for production of a **carotenoid** pigment selected from the group consisting of astaxanthin, adonixanthin, beta-carotene, echinenone, canthaxanthin, zeaxanthin and mixtures

thereof, comprising the steps of:

culturing bacterium strain E-396, FERM BP-4283, or A-581-1, FERM BP-4671, in an aqueous nutrient medium comprising sources of carbon, nitrogen, and inorganic substances and

recovering an individual carotenoid pigment or a mixture of the carotenoid pigments.

Dwg.0/6

L81 ANSWER 15 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN
 ACCESSION NUMBER: 1991-369260 [50] WPIX
 DOC. NO. CPI: C1991-159215
 TITLE: Continuous fermentation of carotenoid
 - producing microorganisms - by addn. of nutrient
 at rate needed for max. growth.
 DERWENT CLASS: D13 D16 E24
 INVENTOR(S): BAILEY, R B; MEDWID, R D
 PATENT ASSIGNEE(S): (COOA) COORS BIOTECH INC; (ZEAG-N) ZEAGEN INC; (UVFO-N)
 UNIVERSAL FOODS CORP; (ARCH) ARCHER-DANIELS MIDLAND CO
 COUNTRY COUNT: 32
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9118108	A	19911128	(199150)*		28
RW: AT BE CH DE DK ES FR GB GR IT LU NL OA SE					
W: AT AU BB BG BR CA CH DE DK ES FI GB HU JP KP KR LK LU MC MW NL NO					
PL RO SD SE SU					
AU 9180820	A	19911210	(199212)		
BR 9106448	A	19930518	(199324)		
EP 553085	A1	19930804	(199331)	EN	28
R: DE ES FR GB GR IT NL					
JP 06500008	W	19940106	(199406)		14
EP 553085	A4	19930901	(199527)		
EP 553085	B1	19991020	(199948)	EN	
R: DE ES FR GB GR IT NL					
DE 69131730	E	19991125	(200002)		
ES 2139577	T3	20000216	(200016)		
JP 3065348	B2	20000717	(200039)		15

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
BR 9106448	A	BR 1991-6448	19910514
		WO 1991-US3358	19910514
EP 553085	A1	EP 1991-910886	19910514
		WO 1991-US3358	19910514
JP 06500008	W	JP 1991-510821	19910514
		WO 1991-US3358	19910514
EP 553085	A4	EP 1991-910886	19910514
EP 553085	B1	EP 1991-910886	19910514
		WO 1991-US3358	19910514
DE 69131730	E	DE 1991-631730	19910514
		EP 1991-910886	19910514
		WO 1991-US3358	19910514
ES 2139577	T3	EP 1991-910886	19910514
JP 3065348	B2	JP 1991-510821	19910514
		WO 1991-US3358	19910514

FILING DETAILS:

PATENT NO	KIND		PATENT NO
BR 9106448	A	Based on	WO 9118108
EP 553085	A1	Based on	WO 9118108
JP 06500008	W	Based on	WO 9118108
EP 553085	B1	Based on	WO 9118108
DE 69131730	E	Based on	EP 553085
		Based on	WO 9118108
ES 2139577	T3	Based on	EP 553085
JP 3065348	B2	Previous Publ.	JP 06500008
		Based on	WO 9118108

PRIORITY APPLN. INFO: US 1990-524140 19900515

AN 1991-369260 [50] WPIX

AB WO 9118108 A UPAB: 19960108

A continuous **fermentation** method for **carotenoid**

-producing heterotrophic microorganisms is claimed comprising (a) diluting a **fermentation** broth comprising the microorganism by continuously adding fresh **fermentation** medium comprising a nutrient to the **fermentation** broth so that the rate of addn. of the nutrient is less than that necessary to provide for a maximum growth rate of the microorganisms, (b) maintaining the pH of the **fermentation** broth at pH 5.5-6.5 and (c) maintaining the temp. at 30-38 deg.C.

The pref. microorganisms are algae of the species *Neosporangiococcum excentricum* (ATCC40355). The nutrient is pref. glucose or sucrose. The **fermentation** broth pref. contains greater than 10% dissolved oxygen and the partial pressure of CO₂ in the broth is pref. less than 0.04.

USE/ADVANTAGE - The process provides a high level of growth and productivity over an extended period of time. In particular, xanthophylls can be produced at levels of at least 20 mg/l/hr. The xanthophylls are useful as natural colouring agents, esp. as feed supplements for poultry. @ (28pp Dwg.No.0/0)

0/0

ABEQ EP 553085 A UPAB: 19931118

A continuous **fermentation** method for **carotenoid**

-producing heterotrophic microorganisms is claimed comprising (a) diluting a **fermentation** broth comprising the microorganism by continuously adding fresh **fermentation** medium comprising a nutrient to the **fermentation** broth so that the rate of addn. of the nutrient is less than that necessary to provide for a maximum growth rate of the microorganisms, (b) maintaining the pH of the **fermentation** broth at pH 5.5-6.5 and (c) maintaining the temp. at 30-38 deg.C.

The pref. microorganisms are algae of the species *Neosporangiococcum excentricum* (ATCC40355). The nutrient is pref. glucose or sucrose. The **fermentation** broth pref. contains greater than 10% dissolved oxygen and the partial pressure of CO₂ in the broth is pref. less than 0.04.

USE/ADVANTAGE - The process provides a high level of growth and productivity over an extended period of time. In particular, xanthophylls can be produced at levels of at least 20 mg/l/hr. The xanthophylls are useful as natural colouring agents, esp. as feed supplements for poultry. Dwg.0/0

L81 ANSWER 16 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 1974-80388V [46] WPIX

TITLE: Deep culturing microorganisms with adequate

oxygen - stirring rate and
oxygen flow adjusted to secure full
oxygen access.

DERWENT CLASS: D16
PATENT ASSIGNEE(S): (KRIK-N) KIRKHENSSTEIN MICROBIOL
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
SU 413183	A	19740528	(197446)*		

PRIORITY APPLN. INFO: SU 1971-1684597 19710727

AN 1974-80388V [46] WPIX

AB SU 413183 A UPAB: 19930831

In the title **culturing** when the air input is 0.3-3.0 vols/vol. medium per min., the stirring rate is increased in steps, and when the exit gas inhibiting CO₂ concn. is 3-11% the stirring rate is cut stepwise with increase also in air supply. In the case of the lysin producer *Brevibacterium* sp. 22, at an air speed 1.2 vols/vol. medium/per min., the stirring rate steps are 180, 230, 280, 330, 380 r.p.m., and when the exit gas CO₂ conc. is 4% the stirrer speed sequence is reversed. With the **carotenoid producer** *Rhodotorula gracilis* Mn, using an air input of 2.0 vols./vol./min., the stirring speeds are 200, 300, 400 r.p.m., then with 11% CO₂ in the exit gas the sequence is reversed.

L81 ANSWER 17 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 1972-39521T [25] WPIX

TITLE: **Carotenoid contg concentrates - microbiological prodn.**

DERWENT CLASS: B04 D16

PATENT ASSIGNEE(S): (KIR-N) INST MIKROBIOLOGII IM AUG

COUNTRY COUNT: 4

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 2059387	A		(197225)*		
GB 1293995	A		(197243)		
FR 2117801	A		(197246)		
JP 49004386	B	19740131	(197409)		

PRIORITY APPLN. INFO: DE 1970-2059387 19701202

AN 1972-39521T [25] WPIX

AB DE 2059387 A UPAB: 19930831

Carotenoid-contg. concentrates useful in the prodn. of fodder prods. and in the food and medicinal inds. are produced by cultivating **carotenoid**-producing micro-organisms under aerobic conditions on a nutrient medium contg. sources of C, N, mineral salts, biologically active substances, stimulants and **carotenoid** precursors until maximal accumulation of the biomass in the **fermentation** medium, effecting a partial separation of the **fermentation** medium from the biomass to give a biomass conc. of is not <50 g (dry wt) per litre of medium, and accumulating **carotenoid** by maintaining the concentrate (optionally after adding carbohydrate and/or trace elements) at 28-35 degrees C and pH 5-7 while aerating at a rate of 80-150 mg

MARX 09/049,228

.02/litre/minute. Fermentati n time is shortened energy requirements are reduced, and the capacity and amt. of equipment required are less.

=> file home

FILE 'HOME' ENTERED AT 12:10:41 ON 28 JUL 2003

MARX 09/049,228

=> d his

(FILE 'HOME' ENTERED AT 10:50:39 ON 28 JUL 2003)

FILE 'HCAPLUS' ENTERED AT 10:50:50 ON 28 JUL 2003.

L1 19 S TSUBOKURA A?/AU
 L2 337 S MIZUTA H?/AU
 L3 354 S L1-2
 L4 8 S L3 AND CAROTENOID
 SELECT RN L4 1-8

FILE 'REGISTRY' ENTERED AT 10:51:40 ON 28 JUL 2003

L5 42 S E1-42
 SAVE TEMP L5 MAR228INV/A

FILE 'HCAPLUS' ENTERED AT 10:51:59 ON 28 JUL 2003

L6 5 S L4 AND L5
 L7 8 S L4 OR L6 *8 cites w/ 42 cpds displayed*

=> d ibib abs hitstr ind 1-8

L7 ANSWER 1 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:924027 HCAPLUS
 DOCUMENT NUMBER: 136:52783
 TITLE: Process for producing carotenoid pigments
 INVENTOR(S): Tsubokura, Akira; Mizuta, Haruyoshi
 PATENT ASSIGNEE(S): Nippon Mitsubishi Oil Corporation, Japan
 SOURCE: PCT Int. Appl., 23 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: Japanese
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001096591	A1	20011220	WO 2001-JP4874	20010608
W: AU, CA, CN, IL, KR, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
JP 2001352995	A2	20011225	JP 2000-175124	20000612
AU 2001062730	A5	20011224	AU 2001-62730	20010608
EP 1229126	A1	20020807	EP 2001-936932	20010608
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
US 2003044886	A1	20030306	US 2002-49228	20020211
PRIORITY APPLN. INFO.:				
			JP 2000-175124	A 20000612
			WO 2001-JP4874	W 20010608

AB A process for the microbial manuf. of carotenoids of desired ratio of carotenoid compds. with bacteria E-396 and A-581-1 which have low growth rate and enable easy isolation of the carotenoids was given: The ratio of the carotenoid compds. (i.e., astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin, zeaxanthin, .beta.-cryptoxanthin, 3-hydroxyechinenone, adonirubin, etc.) is controlled by the concn. of oxygen dissolved in a liq. culture medium during the fermn.

IT 382660-64-2 382660-65-3
 RL: PRP (Properties)
 (nucleotide sequence; process for producing carotenoid pigments)

MARX 09/049,228

RN 382660-64-2 HCAPLUS
CN DNA (bacteria strain E-396 16S ribosomal RNA gene plus flanks) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 382660-65-3 HCAPLUS
CN DNA (bacteria strain A-581-1 16S ribosomal RNA gene plus flanks) (9CI) (CA INDEX NAME)

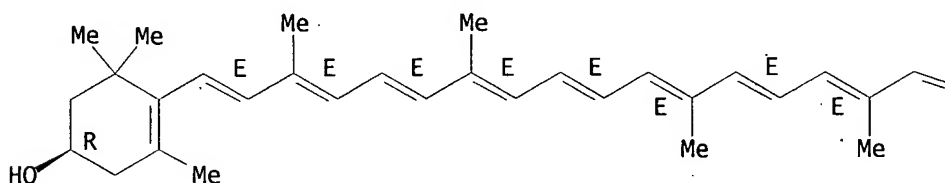
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin
514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone
4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin
7235-40-7P, .beta.-Carotene
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(process for producing carotenoid pigments)

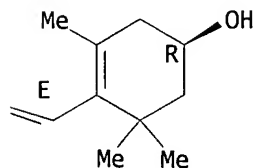
RN 144-68-3 HCAPLUS
CN .beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



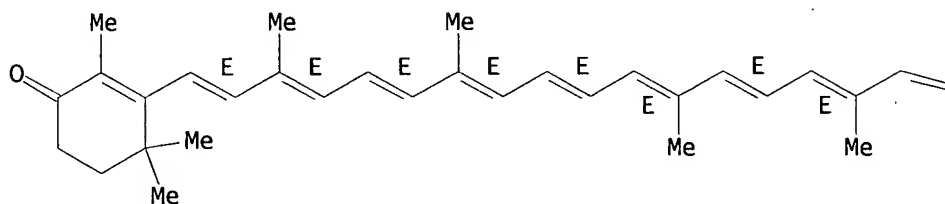
PAGE 1-B



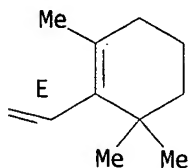
RN 432-68-8 HCAPLUS
CN .beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

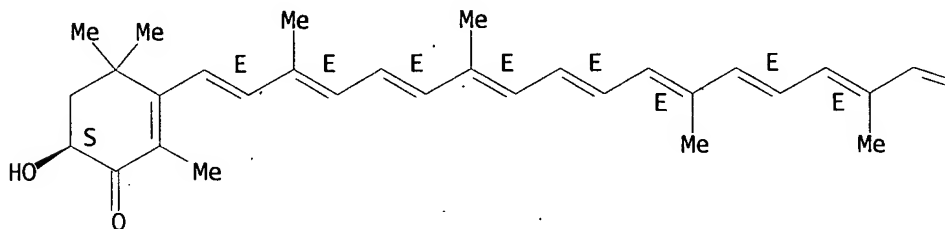


RN 472-61-7 HCAPLUS

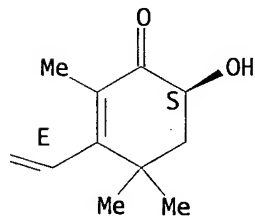
CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

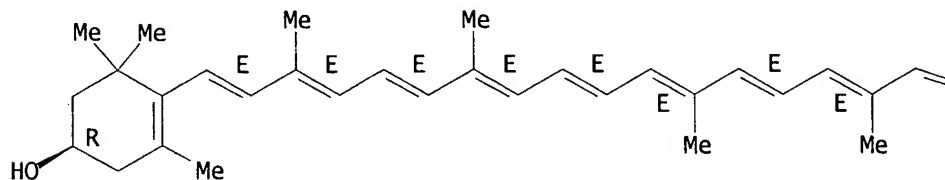


RN 472-70-8 HCAPLUS

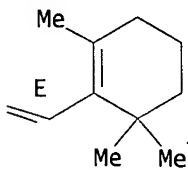
CN .beta.,.beta.-Caroten-3-ol, (3R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

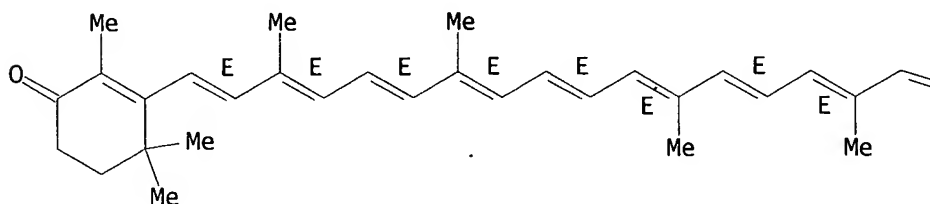


RN 514-78-3 HCAPLUS

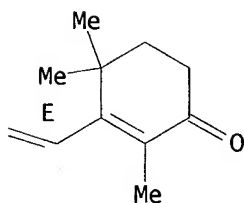
CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

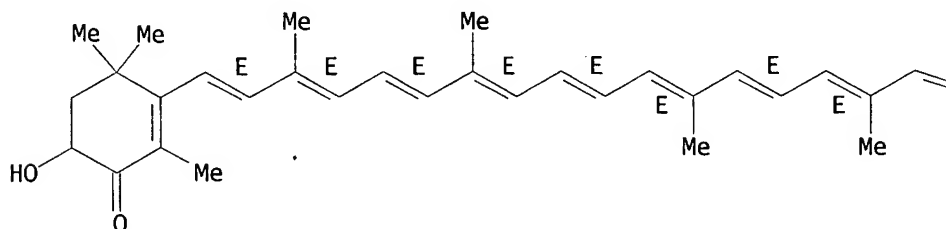


RN 4339-77-9 HCAPLUS

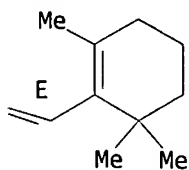
CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

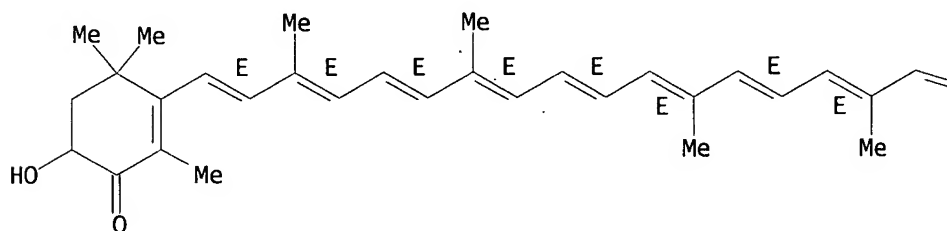


RN 4418-72-8 HCAPLUS

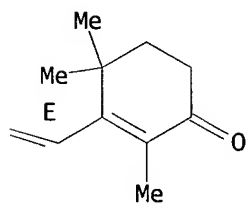
CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

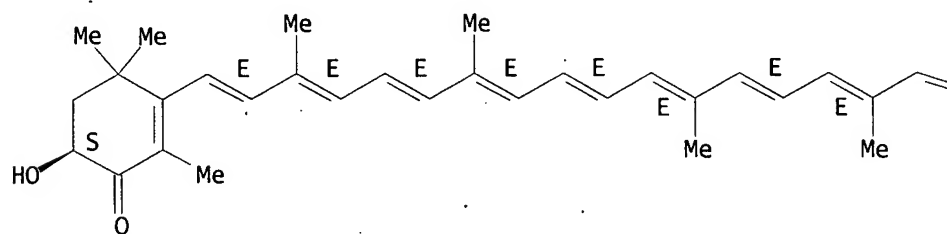


RN 4418-73-9 HCAPLUS

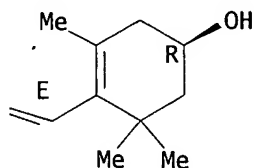
CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



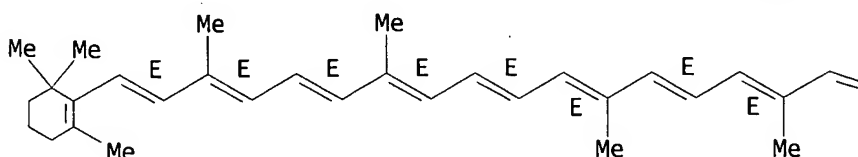
PAGE 1-B



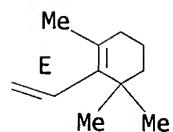
RN 7235-40-7 HCAPLUS
 CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B



IT 7782-44-7, Oxygen, biological studies
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (process for producing **carotenoid** pigments)
 RN 7782-44-7 HCAPLUS
 CN Oxygen (8CI, 9CI) (CA INDEX NAME)

O=O

IC ICM C12P023-00
 CC 16-2 (Fermentation and Bioindustrial Chemistry)
 ST **carotenoid** manuf bacteria dissolved oxygen
 IT rRNA
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (16 S, gene for; process for producing **carotenoid** pigments)
 IT Bacteria (Eubacteria)
 Culture media
 DNA sequences
 Fermentation
 Taxonomy
 (process for producing **carotenoid** pigments)
 IT Carotenes, preparation
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
 (Preparation)
 (process for producing **car tenoid** pigments)
 IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(process for producing **carotenoid** pigments)

IT 382660-64-2 382660-65-3

RL: PRP (Properties)
(nucleotide sequence; process for producing **carotenoid** pigments)

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin
514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone
4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin
7235-40-7P, .beta.-Carotene
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(process for producing **carotenoid** pigments)

IT 7782-44-7, Oxygen, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(process for producing **carotenoid** pigments)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:251697 HCAPLUS

DOCUMENT NUMBER: 134:294933

TITLE: Bacterial **carotenoid**-containing preparations as feed additive

INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Mizuta, Yoshinori

PATENT ASSIGNEE(S): Nisseki Mitsubishi K. K., Japan

SOURCE: Jpn. Kokai Tokkyo Koho, 6 pp.

CODEN: JKXXAF

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2001095500	A2	20010410	JP 1999-279337	19990930
NO 2001002629	A	20010711	NO 2001-2629	20010529
PRIORITY APPLN. INFO.:			JP 1999-279337 A	19990930
			WO 2000-JP6528 W	20000922

AB The preps. comprise ppt. of microbial culture contg. .gtoreq.3% **carotenoids** with astaxanthin content preferably .gtoreq.40%. The microbes are preferably those which contain 16 S rRNA-specifying DNA having sequence substantially homologous to 1452-bp sequence (given). The **carotenoids** are stable to O and light because they are stabilized with cell membrane and cell wall. E-396 (FERM BP-4283) was cultured in a medium contg. yeast ext., peptone, glucose, and salts at 28.degree. for 6 days. The collected cells was dried to give a pigment prepn. (total **carotenoids** 31.2%) contg. .beta.-carotene 1.6, echinenone 1.9, 3-hydroxyechinenone 0.9, canthaxanthin 2.3, adonirubin 5.6, astaxanthin 13.0, asteroideone 0.6, adonixanthin 5.3, and zeaxanthin 0.01%.

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 514-78-3P, Canthaxanthin
4339-77-9P, 3-Hydroxyechinenone 4418-72-8P, Adonirubin
4418-73-9P, Adonixanthin 7235-40-7P, .beta.-Carotene
19866-02-5P, Asteroideone
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD (Food or feed use); BIOL (Biological study); PREP (Preparation); USES

(Uses)

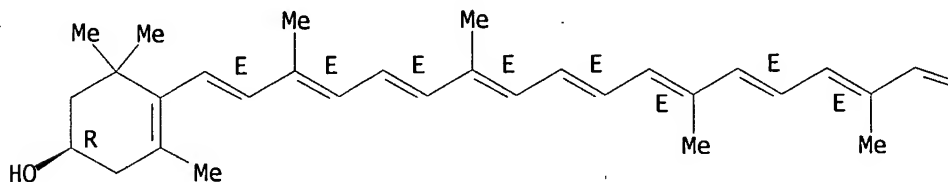
(manuf. of astaxanthin-rich carotenoid-contg. preps. for
feed with microorganisms having specific 16 S rRNA-specifying DNA
sequence)

RN 144-68-3 HCAPLUS

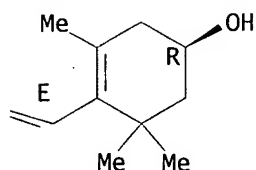
CN .beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

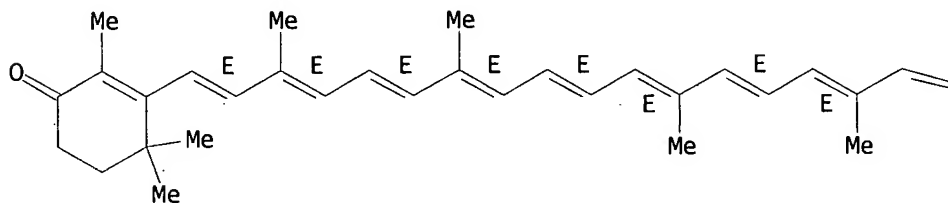


RN 432-68-8 HCAPLUS

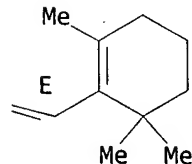
CN .beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

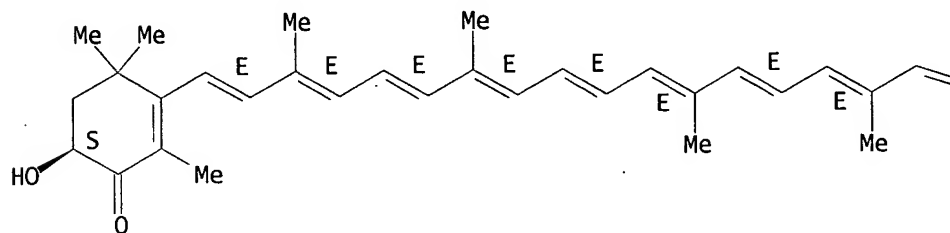


RN 472-61-7 HCAPLUS

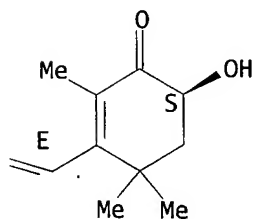
CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



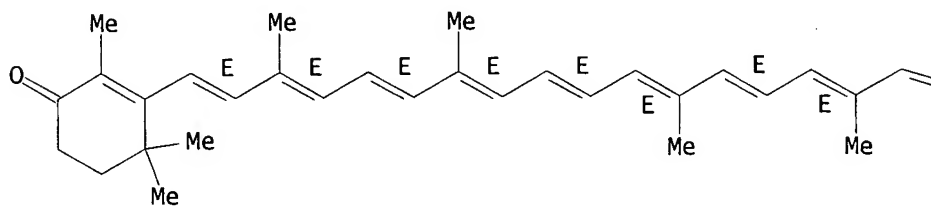
PAGE 1-B



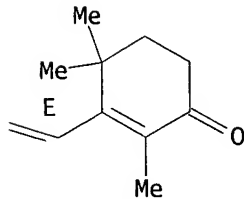
RN 514-78-3 HCAPLUS
CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



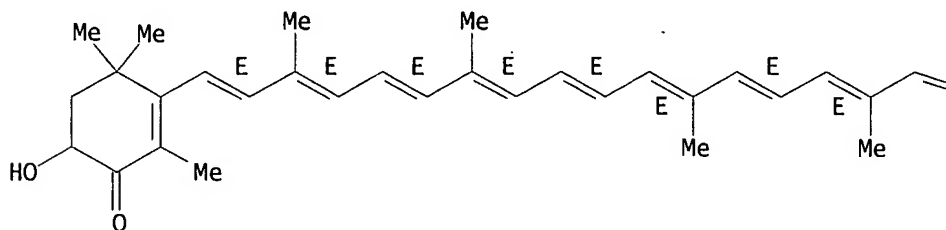
PAGE 1-B



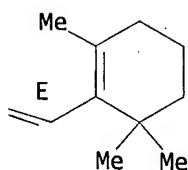
RN 4339-77-9 HCAPLUS
CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

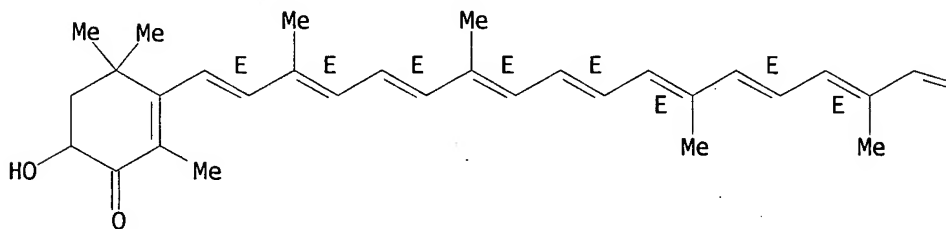


RN 4418-72-8 HCAPLUS

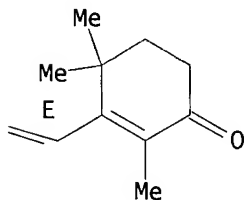
CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

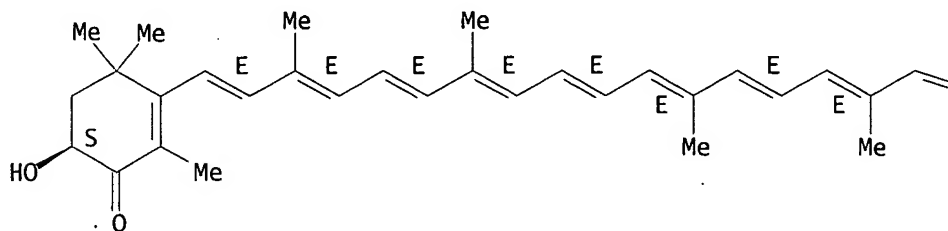


RN 4418-73-9 HCAPLUS

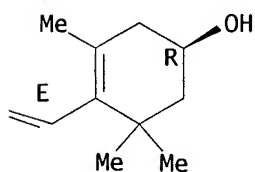
CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



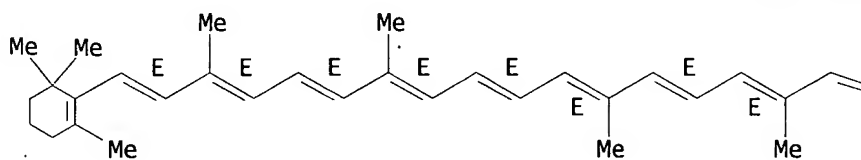
PAGE 1-B



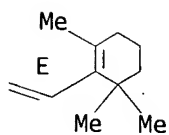
RN 7235-40-7 HCAPLUS
 CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



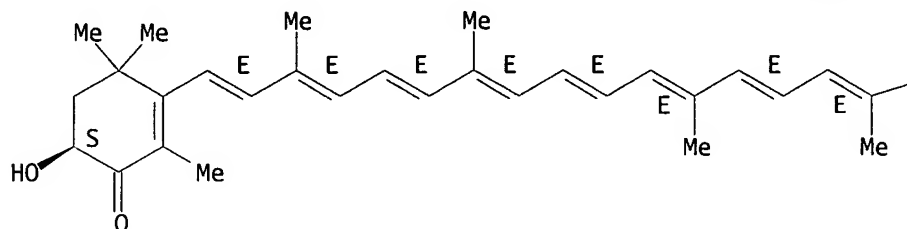
PAGE 1-B



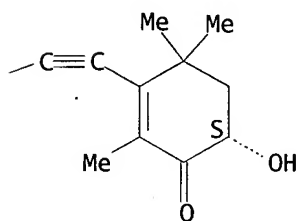
RN 19866-02-5 HCAPLUS
 CN .beta.,.beta.-Carotene-4,4'-dione, 7,8-didehydro-3,3'-dihydroxy-,
 (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
 Double bond geometry as shown.

PAGE 1-A



PAGE 1-B



IT 334071-56-6

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

RN 334071-56-6 HCAPLUS

CN DNA (bacteria strain E-396 16 S rRNA gene) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IC ICM A23K001-16

ICS C09B061-00; C09B067-20; C12N001-20

CC 17-12 (Food and Feed Chemistry)

Section cross-reference(s): 16, 18

ST astaxanthin rich **carotenoid** contg microbial culture feed additive

IT rRNA

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(16 S, DNA for; manuf. of astaxanthin-rich **carotenoid**-contg.

prepns. for feed with microorganisms having specific 16 S

rRNA-specifying DNA sequence)

IT Bacteria (Eubacteria)

(E-396; manuf. of astaxanthin-rich **carotenoid**-contg. prepns.

for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT Feed additives

Fermentation

Pigments, biological

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for

feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT Carotenes, biological studies

RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD

(Food or feed use); BIOL (Biological study); PREP (Preparation); USES

(Uses)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for

feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT DNA

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT

144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 514-78-3P, Canthaxanthin
4339-77-9P, 3-Hydroxyechinenone 4418-72-8P, Adonirubin
4418-73-9P, Adonixanthin 7235-40-7P, .beta.-Carotene
19866-02-5P, Asteroidenone

RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD (Food or feed use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT

334071-56-6

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

L7 ANSWER 3 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:85961 HCAPLUS

DOCUMENT NUMBER: 130:279042

TITLE: Paracoccus carotinifaciens sp. nov., a new aerobic gram-negative astaxanthin-producing bacterium

AUTHOR(S): Tsubokura, Akira; Yoneda, Hisashi; Mizuta, Haruyoshi

CORPORATE SOURCE: Central Technical Research Laboratory, Nippon Oil Company Ltd, Yokohama, 231-0815, Japan

SOURCE: International Journal of Systematic Bacteriology (1999), 49(1), 277-282

CODEN: IJSBA8; ISSN: 0020-7713

PUBLISHER: Society for General Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The strain E-396T, isolated from soil, was Gram-neg., aerobic, orange-pigmented, rod-shaped, motile by peritrichous flagella and astaxanthin-producing. This organism produced **carotenoids**, mainly astaxanthin, and did not produce bacteriochlorophyll. The ubiquinone system was Q-10. Anal. of the 16S rRNA sequence of strain E-396T showed it to be a member of the .alpha.-3 subclass of the Proteobacteria, forming a cluster with the species of the genus Paracoccus. On the basis of the prodn. of orange pigments and motility by peritrichous flagella, together with DNA-DNA reassocn. data, it is concluded that the new isolate should be classified into a new species of the genus Paracoccus, Paracoccus carotinifaciens sp. nov. The type strain is E-396T (= IFO 16121T).

IT

472-61-7, Astaxanthin

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(Paracoccus carotinifaciens sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

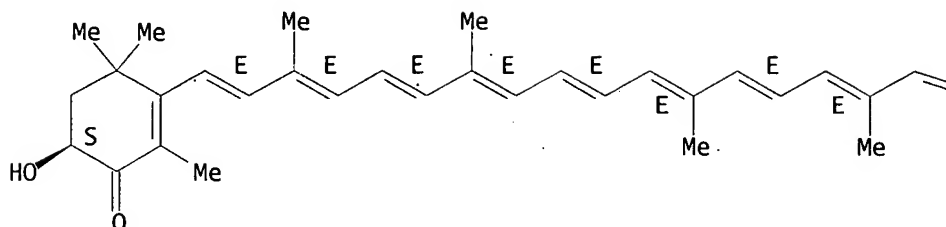
RN 472-61-7 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA

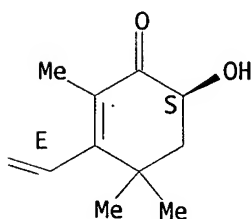
INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B



- IT 222713-29-3
RL: PRP (Properties)
(nucleotide sequence; *Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)
- RN 222713-29-3 HCAPLUS
- CN DNA (*Paracoccus carotinifaciens* strain E-396 16S rRNA gene) (9CI) (CA INDEX NAME)
- *** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
- CC 10-1 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): 3
- ST *Paracoccus carotinifaciens* 16S rRNA gene sequence taxonomy
- IT rRNA
RL: PRP (Properties)
(16 S; *Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)
- IT DNA sequences
Evolution
Paracoccus carotinifaciens
Taxonomy
(*Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)
- IT Gene, microbial
RL: PRP (Properties)
(for 16S rRNA; *Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)
- IT 472-61-7, Astaxanthin
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(*Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg.
astaxanthin-producing bacterium)

IT 222713-29-3

RL: PRP (Properties)

(nucleotide sequence; *Paracoccus carotinifaciens* sp. nov., new aerobic
gram-neg. astaxanthin-producing bacterium)

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:772393 HCAPLUS

DOCUMENT NUMBER: 128:59314

TITLE: Carotenoid-stabilization material

INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Uchiyama,
Yoko; Mizuta, Yoshitaka

PATENT ASSIGNEE(S): Nippon Oil Co., Ltd., Japan

SOURCE: Jpn. Kokai Tokkyo Koho, 14 pp.

CODEN: JKXXAF

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 09308481	A2	19971202	JP 1996-128565	19960523
JP 3278574	B2	20020430		

PRIORITY APPLN. INFO.: JP 1996-128565 19960523

AB The title material (I) is produced by microorganism E-396 or mutant
microorganism A-581-1. I is useful for improvement/stabilization of meat,
egg, and/or skin color. Physiol. and morphol. characteristics of the
microorganism E-396 were given.

IC ICM C12N001-20

ICS A23K001-16; A23K001-18; A23L001-272; C09B061-00; C12N015-09;
C12Q001-68; C12N001-20; C12R001-01

CC 10-1 (Microbial, Algal, and Fungal Biochemistry)

Section cross-reference(s): 16, 17

ST carotenoid stabilization material microorganism fermn

IT Aquaculture

Egg, poultry

Feed additives

Fermentation

Food additives

Health food

Meat

Microorganism

(carotenoid-stabilization material)

IT Carotenes, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
(Biological study); PROC (Process)

(carotenoid-stabilization material)

L7 ANSWER 5 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:338419 HCAPLUS

DOCUMENT NUMBER: 125:9229

TITLE: Process for extraction of carotenoids from
bacterial cellsINVENTOR(S): Kitaoka, Motomitsu; Tsubokura, Akira;
Kiyota, Takashi

PATENT ASSIGNEE(S): Nippon Oil Company, Ltd., Japan

SOURCE: Can. Pat. Appl., 10 pp.
 CODEN: CPXXEB
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CA 2159176	AA	19960328	CA 1995-2159176	19950926
JP 08089280	A2	19960409	JP 1994-231266	19940927
US 5591343	A	19970107	US 1995-533390	19950925
NO 9503813	A	19960328	NO 1995-3813	19950926
EP 719866	A1	19960703	EP 1995-306770	19950926
EP 719866	B1	20011205		

R: CH, DE, FR, GB, LI

PRIORITY APPLN. INFO.: JP 1994-231266 A 19940927

AB A process for extn. of a **carotenoid** compd. from bacterial cells contg. the **carotenoid** compd. comprising the step of bringing the bacterial cells into contact with supercrit. fluid to ext. the **carotenoid** compd. from the cells. The process provides **carotenoid** compds. which can be safely used as feed additives and food additives.

IC ICM C07C403-00
 ICS C07C011-21

CC 17-14 (Food and Feed Chemistry)

ST process extn **carotenoid** bacterial cell

IT Feed
 Food

(additives; process for extn. of **carotenoids** from bacterial cells)

IT Bacteria
 Extraction

(process for extn. of **carotenoids** from bacterial cells)

IT Carotenes and **Carotenoids**, biological studies

RL: FFD (Food or feed use); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation); USES (Uses)

(process for extn. of **carotenoids** from bacterial cells)

IT Fluids

(supercrit., process for extn. of **carotenoids** from bacterial cells)

L7 ANSWER 6 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:153672 HCAPLUS

DOCUMENT NUMBER: 124:198044

TITLE: Novel bacteria producing **carotenoids**

INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Takagi, Mikihiro; Kyota, Takashi

PATENT ASSIGNEE(S): Nippon Oil Co Ltd, Japan

SOURCE: Jpn. Kokai Tokkyo Koho, 20 pp.

CODEN: JKXXAF

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 08009964	A2	19960116	JP 1994-152078	19940704
JP 3429563	B2	20030722		

PRIORITY APPLN. INFO.: JP 1994-152078 19940704
 AB Two novel bacteria capable of producing **carotenoids** are isolated and characterized. FERM BP-4283 strain E-396 and FERM BP-4671 strain A-581-1 are both aerobic, gram-neg. bacteria. A phylogenetic tree of the bacteria is also provided.
 IC ICM C12N001-20
 ICA C12P023-00
 ICI C12N001-20, C12R001-01; C12P023-00, C12R001-01
 CC 10-1 (Microbial, Algal, and Fungal Biochemistry)
 ST bacteria **carotenoid** prodn
 IT Bacteria
 (FERM BP-4283 strain E-396, FERM BP-4671 strain A-581-1; isolation of novel bacteria producing **carotenoids**)
 IT Carotenes and **Carotenoids**, preparation
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
 (isolation of novel bacteria producing **carotenoids**)

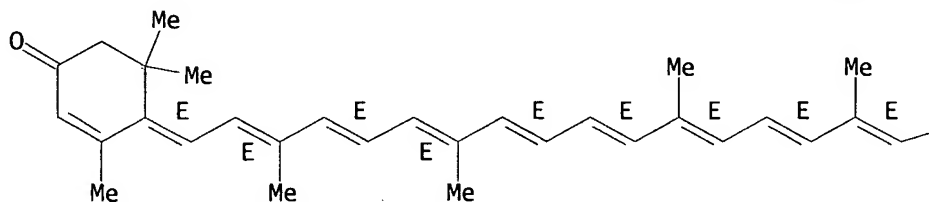
L7 ANSWER 7 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1995:849314 HCAPLUS
 DOCUMENT NUMBER: 123:254690
 TITLE: Process for extracting **carotenoids**
 INVENTOR(S): Kitaoka, Motomitsu; Tsubokura, Akira;
 Kiyota, Takashi
 PATENT ASSIGNEE(S): Nippon Oil Co. Ltd., Japan
 SOURCE: Eur. Pat. Appl., 10 pp.
 CODEN: EPXXDW
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 670306	A1	19950906	EP 1995-102933	19950302
R: CH, DE, FR, GB, LI				
JP 07242621	A2	19950919	JP 1994-32388	19940302
CA 2143689	AA	19950903	CA 1995-2143689	19950301
NO 9500804	A	19950904	NO 1995-804	19950301
PRIORITY APPLN. INFO.:			JP 1994-32388	19940302

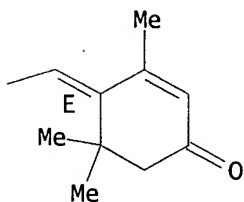
AB A process for extg. **carotenoid** compds. comprising the step of bringing a material contg. the **carotenoid** compd. into contact with a cyclic hydrophilic org. compd. to ext. the **carotenoid** compd. from the material to the cyclic hydrophilic org. compd. By this process, a **carotenoid** compd. can be efficiently extd. resulting in an ext. contg. a high concn. of the **carotenoid** compd.
 IT 116-30-3P 144-68-3P, Zeaxanthin 432-68-8P, Echinenone 432-70-2P, .alpha.-Carotene 472-61-7P, Astaxanthin 472-70-8P, Cryptoxanthin 472-93-5P, .gamma.-Carotene 502-65-8P, Lycopene 514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone 4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin 7235-40-7P, .beta.-Carotene
 RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)
 (extg. **carotenoids**)
 RN 116-30-3 HCAPLUS
 CN 4,5'-retro-.beta.,.beta.-Carotene-3,3'-dione, 4',5'-didehydro- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

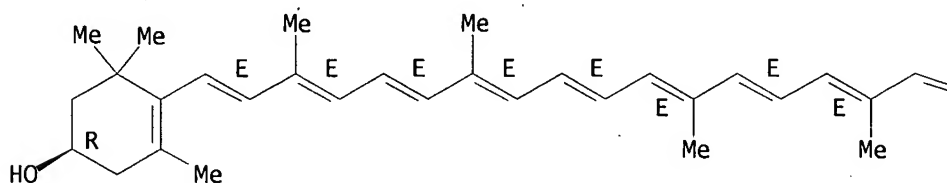


RN 144-68-3 HCAPLUS

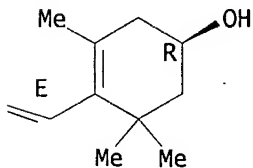
CN .beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

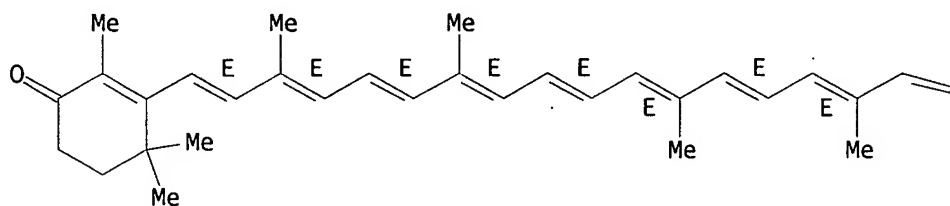


RN 432-68-8 HCAPLUS

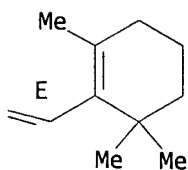
CN .beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



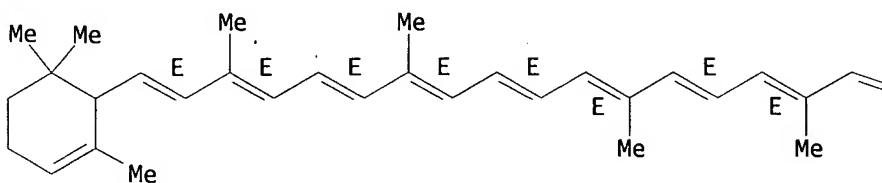
PAGE 1-B



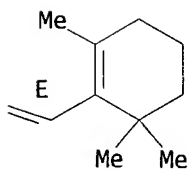
RN 432-70-2 HCAPLUS
 CN .beta.,.epsilon.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



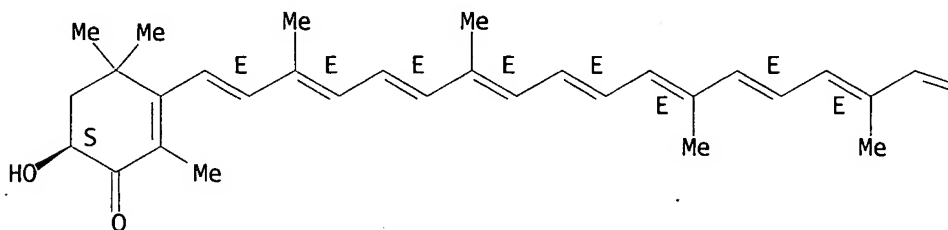
PAGE 1-B



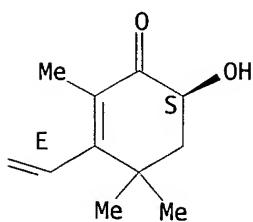
RN 472-61-7 HCAPLUS
 CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
 Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

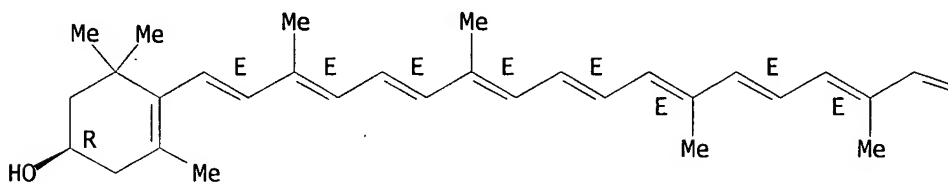


RN 472-70-8 HCAPLUS

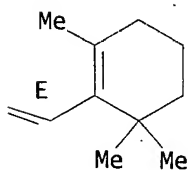
CN .beta.,.beta.-Caroten-3-ol, (3R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

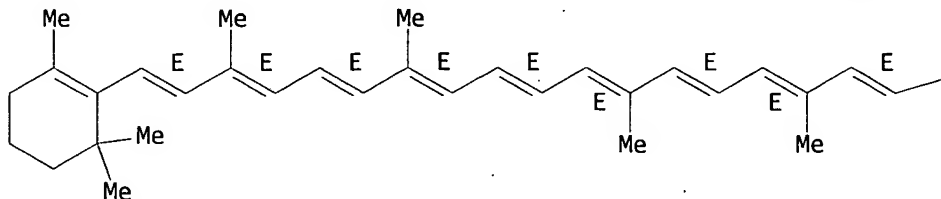


RN 472-93-5 HCAPLUS

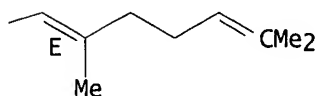
CN .beta.,.psi.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



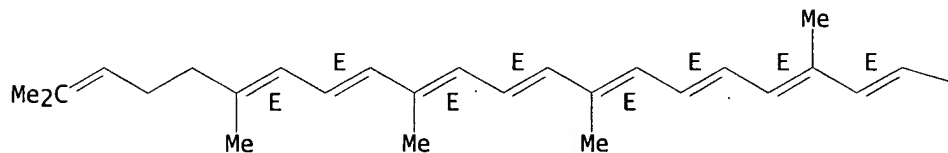
PAGE 1-B



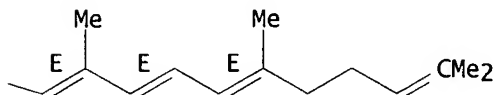
RN 502-65-8 HCAPLUS
 CN .psi.,.psi.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



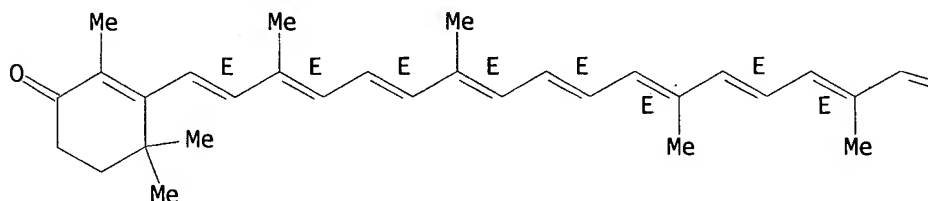
PAGE 1-B



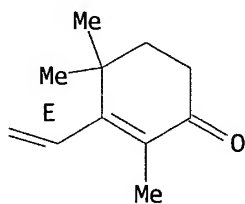
RN 514-78-3 HCAPLUS
 CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

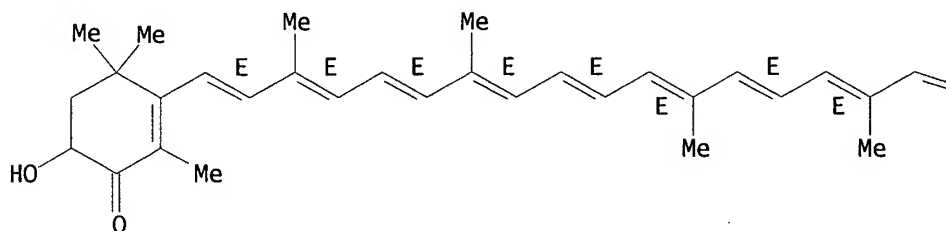


RN 4339-77-9 HCAPLUS

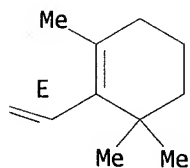
CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

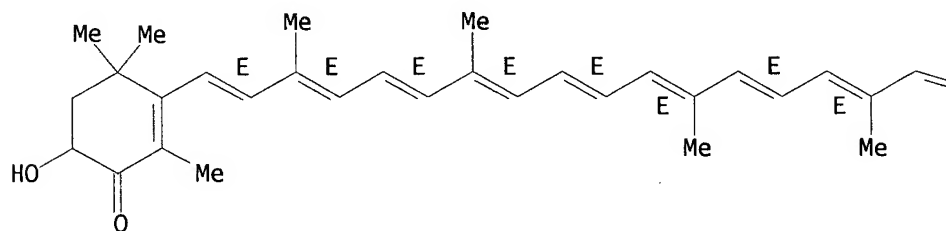


RN 4418-72-8 HCAPLUS

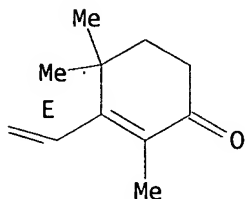
CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

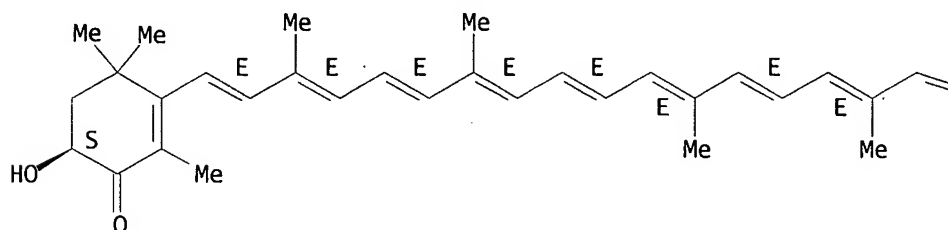


RN 4418-73-9 HCAPLUS

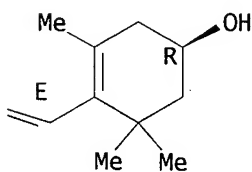
CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

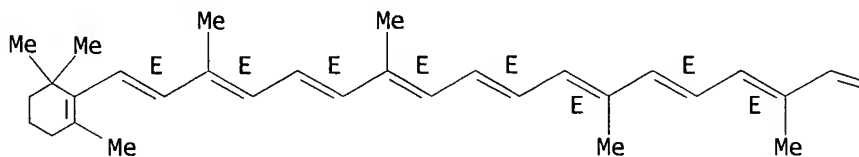


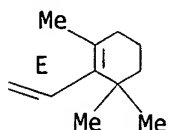
RN 7235-40-7 HCAPLUS

CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



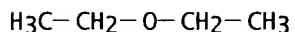


IT 60-29-7, Diethyl ether, uses 64-17-5, Ethanol, uses 67-56-1, Methanol, uses 67-64-1, Acetone, uses 67-66-3, Chloroform, uses 71-23-8, Propanol, uses 71-43-2, Benzene, uses 75-09-2, Dichloromethane, uses 78-93-3, Methyl ethyl ketone, uses 108-20-3, Isopropyl ether 108-88-3, Toluene, uses 108-94-1, Cyclohexanone, uses 109-99-9, THF, uses 110-54-3, Hexane, uses 110-82-7, Cyclohexane, uses 110-86-1, Pyridine, uses 123-86-4, Butyl acetate 123-91-1, Dioxane, uses 141-78-6, Ethyl acetate, uses 142-82-5, Heptane, uses 563-80-4, Methyl isopropyl ketone 1330-20-7, Xylene, uses

RL: NUU (Other use, unclassified); USES (Uses)
(extg. **carotenoids**)

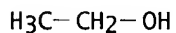
RN 60-29-7 HCAPLUS

CN Ethane, 1,1'-oxybis- (9CI) (CA INDEX NAME)



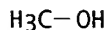
RN 64-17-5 HCAPLUS

CN Ethanol (9CI) (CA INDEX NAME)



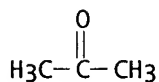
RN 67-56-1 HCAPLUS

CN Methanol (8CI, 9CI) (CA INDEX NAME)



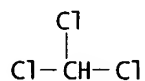
RN 67-64-1 HCAPLUS

CN 2-Propanone (9CI) (CA INDEX NAME)

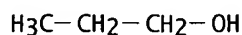


RN 67-66-3 HCAPLUS

CN Methane, trichloro- (9CI) (CA INDEX NAME)



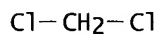
RN 71-23-8 HCAPLUS
CN 1-Propanol (9CI) (CA INDEX NAME)



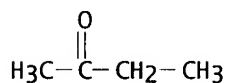
RN 71-43-2 HCAPLUS
CN Benzene (8CI, 9CI) (CA INDEX NAME)



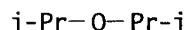
RN 75-09-2 HCAPLUS
CN Methane, dichloro- (8CI, 9CI) (CA INDEX NAME)



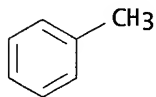
RN 78-93-3 HCAPLUS
CN 2-Butanone (8CI, 9CI) (CA INDEX NAME)



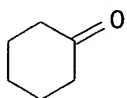
RN 108-20-3 HCAPLUS
CN Propane, 2,2'-oxybis- (9CI) (CA INDEX NAME)



RN 108-88-3 HCAPLUS
CN Benzene, methyl- (9CI) (CA INDEX NAME)



RN 108-94-1 HCAPLUS
CN Cyclohexanone (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 109-99-9 HCAPLUS
CN Furan, tetrahydro- (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 110-54-3 HCAPLUS
CN Hexane (8CI, 9CI) (CA INDEX NAME)

Me-(CH₂)₄-Me

RN 110-82-7 HCAPLUS
CN Cyclohexane (8CI, 9CI) (CA INDEX NAME)



RN 110-86-1 HCAPLUS
CN Pyridine (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 123-86-4 HCAPLUS
CN Acetic acid, butyl ester (8CI, 9CI) (CA INDEX NAME)

n-Bu-O-Ac

RN 123-91-1 HCAPLUS
CN 1,4-Dioxane (9CI) (CA INDEX NAME)



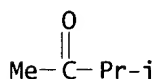
RN 141-78-6 HCAPLUS
CN Acetic acid ethyl ester (8CI, 9CI) (CA INDEX NAME)

Et-O-Ac

RN 142-82-5 HCAPLUS
 CN Heptane (8CI, 9CI) (CA INDEX NAME)

Me-(CH₂)₅-Me

RN 563-80-4 HCAPLUS
 CN 2-Butanone, 3-methyl- (8CI, 9CI) (CA INDEX NAME)



RN 1330-20-7 HCAPLUS
 CN Benzene, dimethyl- (9CI) (CA INDEX NAME)



2 (D1-Me)

IC ICM C07C403-24
 ICS C12P023-00
 CC 16-1 (Fermentation and Bioindustrial Chemistry)
 ST **carotenoid** fermn extn
 IT Algae
 Bacteria
 Corynebacterium
 Dunaliella
 Fermentation
 Haematococcus pluvialis
 Phaffia rhodozyma
 (carotenoid extn. from)
 IT Carotenes and **Carotenoids**, preparation
 RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL
 (Biological study); PREP (Preparation)
 (extg. **carotenoids**)
 IT Ligroine
 RL: NUU (Other use, unclassified); USES (Uses)
 (extg. **carotenoids**)
 IT 116-30-3P 144-68-3P, Zeaxanthin 432-68-8P,
 Echinenone 432-70-2P, .alpha.-Carotene 472-61-7P,
 Astaxanthin 472-70-8P, Cryptoxanthin 472-93-5P,
 .gamma.-Carotene 502-65-8P, Lycopene 514-78-3P,
 Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone 4418-72-8P,
 , Adonirubin 4418-73-9P, Adonixanthin 7235-40-7P,
 .beta.-Carotene

RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)

(extg. **carotenoids**)

IT 60-29-7, Diethyl ether, uses 64-17-5, Ethanol, uses 67-56-1, Methanol, uses 67-64-1, Acetone, uses 67-66-3, Chloroform, uses 71-23-8, Propanol, uses 71-43-2, Benzene, uses 75-09-2, Dichloromethane, uses 78-93-3, Methyl ethyl ketone, uses 108-20-3, Isopropyl ether 108-88-3, Toluene, uses 108-94-1, Cyclohexanone, uses 109-99-9, THF, uses 110-54-3, Hexane, uses 110-82-7, Cyclohexane, uses 110-86-1, Pyridine, uses 123-86-4, Butyl acetate 123-91-1, Dioxane, uses 141-78-6, Ethyl acetate, uses 142-82-5, Heptane, uses 563-80-4, Methyl isopropyl ketone 1330-20-7, Xylene, uses

RL: NUU (Other use, unclassified); USES (Uses)

(extg. **carotenoids**)

L7 ANSWER 8 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:489962 HCAPLUS

DOCUMENT NUMBER: 122:289068

TITLE: Bacteria belonging to new genus and process for production of **carotenoids** using same.

INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Takaki, Mikihiro; Kiyota, Takashi

PATENT ASSIGNEE(S): Nippon Oil Co., Ltd., Japan

SOURCE: Eur. Pat. Appl., 29 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 635576	A1	19950125	EP 1994-111525	19940722
EP 635576	B1	20000830		
R: CH, DE, FR, GB, LI				
JP 07079796	A2	19950328	JP 1994-152240	19940704
JP 3242531	B2	20011225		
US 5607839	A	19970304	US 1994-276943	19940719
CA 2128549	AA	19950123	CA 1994-2128549	19940721
NO 9402731	A	19950123	NO 1994-2731	19940721
US 5858761	A	19990112	US 1996-716841	19960919

PRIORITY APPLN. INFO.: JP 1993-181615 A 19930722

US 1994-276943 A3 19940719

AB Bacterium belonging to a new genus, and a process for prodn. of **carotenoid** pigment selected from the group consisting of astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin and zeaxanthin, comprising the steps of culturing a bacterium capable of producing at least one of the **carotenoid** pigments, and recovering an individual **carotenoid** pigments. The producer bacterium belongs to new genus. According to the present process various **carotenoids** can be produced in an industrial scale. By the present process (3S, 3'S)-astaxanthin can be produced in an almost 100% purity.

IT 472-61-7, (3S, 3'S)-Astaxanthin 4418-73-9, Adonixanthin

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(bacteria belonging to new genus and process for prodn. of

MARX 09/049,228

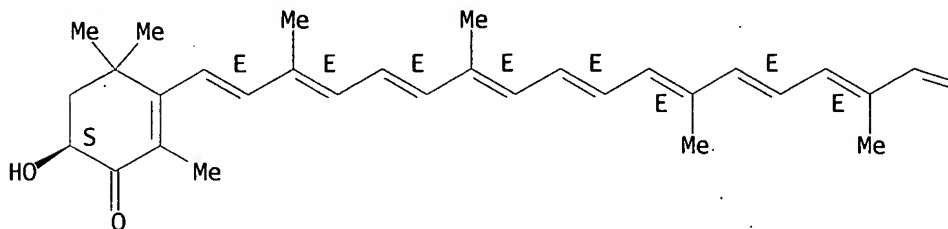
carotenoids using same)

RN 472-61-7 HCAPLUS

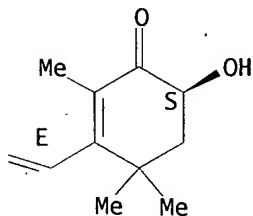
CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

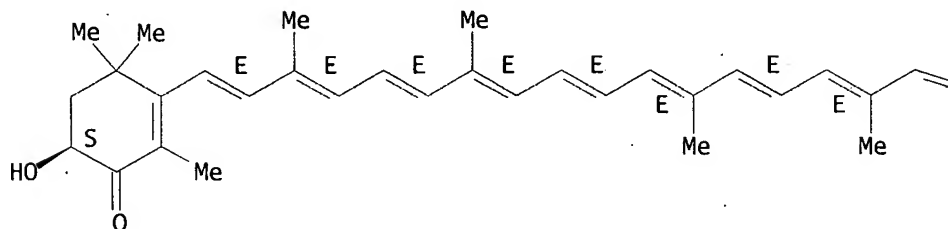


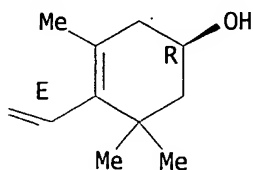
RN 4418-73-9 HCAPLUS

CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A





IT 162875-45-8

RL: PRP (Properties)

(nucleotide sequence of; bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

RN 162875-45-8 HCAPLUS

CN DNA (bacterium strain E-396 16S rRNA gene) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IC ICM C12P025-00

ICS C12N001-20

CC 16-5 (Fermentation and Bioindustrial Chemistry)

ST **carotenoid** formation bacteria; astaxanthin formation bacteria; adonixanthin formation bacteria; rRNA 16S gene sequence bacteria

IT Bacteria

Deoxyribonucleic acid sequences

(bacteria belonging to new genus and process for prodn. of **carotenoids** using same)IT Carotenes and **Carotenoids**, biological studies

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT Gene, microbial

RL: PRP (Properties)

(bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT Ribonucleic acids, ribosomal

RL: PRP (Properties)

(16 S, bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT 472-61-7, (3S, 3'S)-Astaxanthin 4418-73-9, Adonixanthin

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT 162875-45-8

RL: PRP (Properties)

(nucleotide sequence of; bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 09:18:53 ; Search time 5293 Seconds
(without alignments)
11222.516 Million cell updates/sec

Title: US-10-049-228-1

Perfect score: 1452

Sequence: 1 agttgatccgtgctcagaa.....tgcgctggtacacacctctt 1452

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.pl.*
8: gb.pr.*
9: gb.pr.*
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11: gb.sts.*
12: gb.sv.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.mu.*
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22: em.ov.*
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24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
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39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	1451	99.9	1452	6	AR028747	AR028747 Sequence
3	1451	99.9	1452	6	BD093842	BD093842 A pigment
4	1451	99.9	1452	6	BD102673	BD102673 A process
5	1451	99.9	1452	6	E14335	E14335 DNA encodin
6	1451	99.9	1452	6	E40922	E40922 Material co
7	1451	99.9	1452	6	I36531	I36531 Sequence 1
8	1414.8	97.4	1430	1	PM16SRNN	Y12703 Paracoccu
9	1380	95.0	1426	6	BD102674	BD102674 A process
10	1344.8	92.6	1360	1	AB008114	AB008114 Paracoccu
11	1343.8	92.5	1408	1	AB025190	AB025190 Paracoccu
12	1341.2	92.4	1456	1	AY014177	AY014177 Paracoccu
13	1340.2	92.3	1460	1	AY014169	AY014169 Paracoccu
14	1338.6	92.2	1461	1	AY014170	AY014170 Paracoccu
15	1335.6	92.0	1453	1	AY014168	AY014168 Paracoccu
16	1329.6	91.6	1420	1	PAL294415	AJ294415 Paracoccu
17	1328.6	91.5	1409	1	AB025192	AB025192 Paracoccu
18	1325.2	91.3	1416	1	PSE428275	AJ428275 Paracoccu
19	1324.4	91.2	1458	1	AY014176	AY014176 Paracoccu
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21	1316.2	90.6	1462	1	AY014171	AY014171 Paracoccu
22	1308.6	90.1	1458	1	PSP012067	AY012067 Paracoccu
23	1306.6	90.0	1453	1	AB098589	AB098589 Paracoccu
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33	1285.2	88.5	1349	1	PSP391198	AJ391198 Paracoccu
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35	1285.2	88.5	1404	6	AX701408	AX701408 Sequence
36	1280	88.2	1418	1	AF376134	AF376134 Paracoccu
37	1278.4	88.0	1434	1	PSP244715	AJ244715 Paracoccu
38	1274.2	87.8	1385	1	PDEJCM736A	D32238 Paracoccu
39	1273	87.7	1377	1	AF529328	AF529328 Unculture
40	1271.4	87.6	1403	1	AF229874	AF229874 Paracoccu
41	1271	87.5	1385	1	PDEJCM768B	D32239 Paracoccu
42	1270.2	87.5	1389	1	AB018688	AB018688 Paracoccu
43	1266.4	87.2	1457	1	AY014174	AY014174 Paracoccu
44	1263.8	87.0	1389	1	AB008115	AB008115 Paracoccu
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ALIGNMENTS

RESULT 1	AB006899	AB006899	1452 bp	DNA	linear	BCT 10-MAR-1999
LOCUS	Paracoccus	carotinifaciens	gene for 16S rRNA,	complete	sequence.	
DEFINITION	AB006899					
ACCESSION	AB006899					
VERSION	AB006899.1	GI:4514305				
KEYWORDS	16S ribosomal RNA					
SOURCE	Paracoccus carotinifaciens					
ORGANISM	Paracoccus carotinifaciens					
REFERENCE	1 (sites)					
Tsubokura,A., Yoneda,H. and Mizuta,H.						
Paracoccus carotinifaciens sp. nov., a new aerobic gram-negative						
astaxanthin-producing bacterium						

Pred. No. is the number of results predicted by chance to have a

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901	QY	AAGCGCAGAACTTTACCAACCTTTGACATGCGACGACCGCTGGAGAGATTCAGCTTTCT	960
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1 (bases 1 to 1452)	AUTHORS		
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Bacteria for production of carotenoids	JOURNAL		
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DEFINITION A process for producing carotenoid pigments.
ACCESSION BD102673
VERSION BD102673.1 GI:22648247
KEYWORDS WO 0196591-A/1.
SOURCE unidentified
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REFERENCE 1 (bases 1 to 1452)
AUTHORS Tsubokura,A. and Mizuta,H.
TITLE A process for producing carotenoid pigments
JOURNAL Patent: WO 0196591-A 1 20-DEC-2001;
NIPPON MITSUBISHI OIL CORP,AKIRA TSUBOKURA,HARUYOSHI MIZUTA
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VERSION E14335.1 GI:5709018
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SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1452)
AUTHORS Tsubokura, A., Yoneda, H., Uchiyama, Y. and Mizuta, Y.
TITLE COLOR TONE IMPROVER
JOURNAL Patent: JP 1997308481-A 1 02-DEC-1997;
NIPPON OIL CO LTD
COMMENT OS Unknown
PN JP 1997308481-A/1
PD 02-DEC-1997
PF 23-MAY-1996 JP 1996128565
PI Tsubokura AKIRA, YONEDA HISASHI, UCHIYAMA YOKO, PI MIZUTA YOSHINORI
PC C12N1/20,A23K1/16,A23K1/18,A23K1/18,A23L1/272, PC
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Best Local Similarity 100.0%; Pred. No. 0;
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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unidentified
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PD 30-SEP-1999 JP 1999279337
PI AKIRA Tsubokura, HISASHI YONEDA, YOSHITAKA MIZUTA PC
A23K1/16, C09B61/00, C09B67/20, C12N1/20
CC
FH Location/Qualifiers.

FEATURES
source

BASE COUNT 353 a 346 c 461 g 291 t 1 others.

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Best Local Similarity 100.0%; Pred. No. 0;
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ACCESSION I36531
VERSION I36531.1 GI:2086356
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1452)
AUTHORS Tsubokura, A., Yoneda, H., Takaki, M. and Kiyota, T.
TITLE Bacteria belonging to new genus process for production of carotenoids using same
JOURNAL Patent: US 5607839-A 1 04-MAR-1997;
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VERSION Y12703.1 GI:2765222
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ORGANISM Paracoccus marcusii
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
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REFERENCE 1

AUTHORS Harker, M., Hirschberg, J. and Oren, A.
TITLE Paracoccus marcusii sp. nov., an orange gram-negative coccus
JOURNAL Int. J. Syst. Bacteriol. 48 Pt 2, 543-548 (1998)
MEDLINE 98401483
PUBMED 9731296
REFERENCE 2 (bases 1 to 1430)
AUTHORS Hirschberg, J.
TITLE Direct Submission
JOURNAL Submitted (21-APR-1997) J. Hirschberg, The Hebrew University of
Jerusalem, Dept of Genetics, Givat Ram, Jerusalem 91904, ISRAEL
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LOCUS
DEFINITION A process for producing carotenoid pigments.
ACCESSION BD102674
VERSION BD102674.1 GI:22648248
KEYWORDS WO 0196591-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1426)
AUTHORS Tsubokura, A. and Mizuta, H.
TITLE A process for producing carotenoid pigments
JOURNAL Patent: WO 0196591-A 2 20-DEC-2001;
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COMMENT OS Unknown
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PD 20-DEC-2001
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PR 12-JUN-2000 JP OOP 175124
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LOCUS
DEFINITION Paracoccus sp. MBIC1143 gene for 16S rRNA, partial sequence.
ACCESSION AB008114
VERSION AB008114.1 GI:4512342
KEYWORDS
SOURCE Paracoccus sp. MBIC1143
ORGANISM Paracoccus sp. MBIC1143
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
Rhodobacteraceae; Paracoccus.
REFERENCE
1 Misawa,N., Satomi,Y., Kondo,K., Yokoyama,A., Kajiwara,S., Saito,T.,
Ohtani,T. and Miki,W.
Structure and functional analysis of a marine bacterial carotenoid
biosynthesis gene cluster and astaxanthin biosynthetic pathway
proposed at the gene level
J. Bacteriol. 177 (22), 6575-6584 (1995)
96062243
7592436
REFERENCE
2 Hamada,T., Yokoyama,A. and Harayama,S.
Paracoccus aurantiacus gen. nov., sp. nov., a new Carotenoid
Astaxanthin producing marine bacteria
Unpublished
3 (bases 1 to 1360)
Hamada,T.
Direct Submission
Submitted (14-OCT-1997) Tohru Hamada, Marine Biotechnology
Institute, Kamaishi Laboratories; 3-75-1 Heita, Kamaishi, Iwate
026-0001, Japan (E-mail:thamada@mano-enzyme.ne.jp,
Tel:++81-193-26-6538, Fax:++81-193-26-6592)
Location/Qualifiers
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/db_xref="taxon:81397"
/note="synonymous name given at accession:Agrobacterium
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ACCESSION AB025190
VERSION AB025190.1 GI:4586609
KEYWORDS 16S rRNA; 16S ribosomal RNA.
SOURCE Paracoccus sp. MBIC4019
ORGANISM Paracoccus sp. MBIC4019
          Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
          Rhodobacteraceae; Paracoccus.
REFERENCE 1
AUTHORS Hamada,T.
TITLE Identification and Classification of Alpha Proteobacteria
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1408)
AUTHORS Hamada,T.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1999) Tohru Hamada, Marine Biotechnology
          Institute, Kamaiishi Laboratories; 3-75-1 Heita, Kamaiishi, Iwate
          026-0001, Japan (E-mail:thamada@mano-enzyme.ne.jp,
          Tel:81-193-26-6538, Fax:81-193-26-6592)
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LOCUS 1456 bp DNA linear BCT.10-MAR-2003
DEFINITION Paracoccus alcaliphilus 16S ribosomal RNA gene, partial sequence.
ACCESSION AY014177
VERSION AY014177.1 GI:13489271
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SOURCE Paracoccus alcaliphilus
ORGANISM Paracoccus alcaliphilus
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
1 (bases 1 to 1456)
Daneshvar,M.I., Hollis,D.G., Weyant,R.S., Steigerwalt,A.G.,
Whitney,A.M., Douglas,M.P., Macgregor,J.P., Jordan,J.G.,
Mayer,L.W., Rassouli,S.M., Marchet,W., Munro,C., Shuttleworth,L.
and Bernard,K.
Paracoccus yeeli sp. nov. (Formerly CDC Group EO-2), a Novel
Bacterial Species Associated with Human Infection
J. Clin. Microbiol. 41 (3), 1289-1294 (2003)
12624070
2 (bases 1 to 1456)
Douglas,M.P., Weyant,R.S., Hollis,D.G., Jordan,J., Macgregor,J.,
Steigerwalt,A.G. and Daneshvar,M.I.
Direct Submission
Submitted (16-Nov-2000) NCID/DBMD/MSBP/SBRL, Centers for Disease
Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, USA
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RESULT 15
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sequence.
ACCESSION AY014168
VERSION AY014168.1 GI:13489262
KEYWORDS
SOURCE Paracoccus yeeli
ORGANISM Paracoccus yeeli
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
REFERENCE 1 (bases 1 to 1453)
AUTHORS Daneshvar,M.I., Hollis,D.G., Weyant,R.S., Steigerwalt,A.G.,
Whitney,A.M., Douglas,M.P., Macgregor,J.P., Jordan,J.G.,
Mayer,L.W., Rassouli,S.M., Barchet,W., Munro,C., Shuttlesworth,L.
and Bernard,K.
TITLE Paracoccus yeeli sp. nov. (Formerly CDC Group EO-2), a Novel
Bacterial Species Associated with Human Infection
J. Clin. Microbiol. 41 (3), 1265-1294 (2003)
PUBMED 12624070
REFERENCE 2 (bases 1 to 1453)
AUTHORS Douglas,M.P., Weyant,R.S., Hollis,D.G., Jordan,J., Macgregor,J.,
Steigerwalt,A.G. and Daneshvar,M.I.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) NCID/DBMD/MSBP/SBRL, Centers for Disease
Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, USA
FEATURES
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BASE COUNT 355 a 349 c 461 g 288 t
ORIGIN

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Best Local Similarity 95.9%; Pred. No. 0;
Matches 1393; Conservative 0; Mismatches 55; Indels 5; Gaps 2;

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Db 61 CTTTCGGGTACGCGGCGGACGGGTGAGTAACGCTGGGACGCTGCCCTTCTCTACGGAAT 120
QY 124 AGCCCCGGGAACTGGGAGTAATACCGTATACCCCTTTGGGGGAAAGATTTATCGGAGA 183
Db 121 AGCCCTGGGAACTGGGAGTAATACCGTATACCCCTTATTTGGGGAAAGATTTATCGGAGA 180

QY 184 AGGATCGGCCCGCTTGGATTAGGTAGTGGGGTAAATGGCCCAACCAAGCCGACGATC 243
Db 181 AGGATCAGCCCGCTTGGATTAGGTAGTGGGGTAAATGGCCCAACCAAGCCGACGATC 240
QY 244 CATAGCTGGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCGACGATCCTA 303
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Db 1200 CATCTCAGTTCGATGCTCTCTGCAACTCGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1259
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|||||
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Db 1320 ATGGGAGTTGGTCTACCGGACGCGCGTGCGCCAACCTGCGCAAGAGAGGCGCAGCGGACCA 1379
QY 1380 CCGTAGGATCAGCGACTGGGGTGAAGTCGTAAAGGTAGCCGTAGGGGAACCTGCGGCT 1439
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QY 1440 GGATCACCTCCTT 1452
Db 1440 GGATCACCTCCTT 1452

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model.

Run on: July 28, 2003, 09:18:53 ; Search time 350 Seconds
(without alignments)
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Title: US-10-049-228-1

Perfect score: 1452

Sequence: 1 agttgtatctgctgcagaa.....tcggctggtgacactcctt 1452

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Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1451	99.9	1452	17	AA115842
2	1451	98.9	1452	19	AAV22896
3	1451	99.9	1452	22	AAF82204
4	1451	99.9	1452	24	ABL40151
5	1439	99.1	1451	16	AAQ81791
6	1414.8	97.4	1430	20	AAQ07384
7	1380	95.0	1426	24	ABL40152
8	1246.2	85.8	1452	24	ABL55950

DNA derived from 1
DNA encoding a col
DNA sequence used
16S ribosomal RNA
Nucleotide sequenc
Paracoccus marcusii
16S ribosomal RNA
Rhodobacter sphaer

9	1246.2	85.8	1462	24	ABL55996
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16	1098.6	75.7	1405	22	AAH49546
17	1093.6	75.3	1466	22	AAH11032
18	1086.4	74.8	1502	20	AAV72293
19	1082.6	74.6	1450	22	AAV90275
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21	1024.4	70.6	1446	17	AAV10955
22	1002.4	69.0	1446	25	ABZ26100
23	1002.4	69.0	1450	20	AAH82005
24	987.4	68.0	1556	20	AAH81995
25	973.6	67.1	1436	21	AAZ45683
26	969.8	66.8	1479	24	ABS71617
27	969.2	66.7	1321	24	ABL55948
28	967.6	66.6	1319	24	ABL55994
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30	967.6	66.6	1319	24	ABL55995
31	960.4	66.1	1438	21	AAZ45682
32	947.6	65.3	1500	22	AAH89988
33	939.4	64.7	1360	22	AAH89982
34	939.2	64.7	1225	22	AAH89990
35	937.2	64.5	1500	22	AAH89980
36	936	64.5	1361	22	AAH90021
37	929	64.0	1223	22	AAH89985
38	928.4	63.9	1535	20	AAH83569
39	920.2	63.4	1237	22	AAH89986
40	918.8	63.3	1535	20	AAH83568
41	916.4	63.1	1528	20	AAH83570
42	906	62.4	1346	22	AAH89987
43	904.8	62.3	1208	20	AAV72292
44	900.6	62.0	1288	22	AAH89983
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ALIGNMENTS

RESULT 1
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ID AA115842 standard; DNA; 1452 BP.
XX
AC AA115842;
XX
DT 15-AUG-1996 (first entry)
XX
DE DNA derived from 16S ribosomal RNA.
XX
KW 16S rRNA; E-396 (FERM BP-4283); A-581-1 (FERM BP-4671);
KW all-trans astaxanthin; ss;
XX
OS E-396 (FERM BP-4283).
XX
PN JP08009964-A.
XX
PD 16-JAN-1996.
XX
PF 04-JUL-1994; 94JP-0152078.
XX
PR 04-JUL-1994; 94JP-0152078.
XX
PA (NIOC) NIPPON OIL CO LTD.
XX
DR WPI; 1996-110265/12.
XX
PT New microbes E-396 and A-581-1 - useful for prodn. of all-trans
XX astaxanthin
XX
PS Disclosure; Page 17-18; 20pp; Japanese.

xx This sequence represents the 16S rRNA gene from a new species of
cc microbe, E-396 (FERM BP-4283). The microbe is a gram negative
cc pleomorphic rod shaped motile microbe which is aerobic. The GC
cc content of the intracellular DNA is 64-69%. The microbe may be used
cc in the production of all-trans astaxanthin in high yield.
xx
xx
sq sequence 1452 BP; 353 A; 346 C; 461 G; 291 T; 1 other;

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Query Match . 99.9%; Score 1451; DB 17; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	541	AAATCCAGGGCTCAACCTTTGGAACCTGCCCTTTGGAACCTATCAGTCTCGAGTTCGAGAGAG	600
Qy	601	GTGAGTGGAAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGAGAGAACCAACGATGGC	660
Db	601	GTGAGTGGAAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGAGAGAACCAACGATGGC	660
Qy	661	GAAGCGGCTCAGTCGGCTCGATCTGACGCTGAGGTGGAAGCGTGGGAGGCAACAGG	720
Db	661	GAAGCGGCTCAGTCGGCTCGATCTGACGCTGAGGTGGAAGCGTGGGAGGCAACAGG	720
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Qy	841	AACTCAAGGAATTAGCGGGGCCCCGACAAAGCGGTGAGGATGTGGTTTAATTTCGAAGC	900
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Qy	901	AACGCGAGAACTTACCAACCCCTTGACATGGCAGACCGCTGGAGAGATTACGCTTTCT	960
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Db	961	CGTAAAGAGACCTGCACACAGGTGCTGCATGGCTGTCGTGAGTCTGTCGTGAGATGTTTC	1020
Qy	1021	GGTTAAGTCGCGCAACGAGCGCAACCACGTCCTAGTTGCCAGCAATTCAGTTGGGAAC	1080
Db	1021	GGTTAAGTCGCGCAACGAGCGCAACCACGTCCTAGTTGCCAGCAATTCAGTTGGGAAC	1080
Qy	1081	TCTATGGAACCTGCCGATGATAGTGGAGGAAGTGTGGATGACGTCAAGTCTCTATGG	1140
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Qy	1141	GCCTTACGGCTGGGCTACACAGTGTCTACAAATGGTGTGACAGTGGTGTAAATCCCAAA	1200
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Qy	1201	AGCCATCTCAGTTCCGGAATTCCTCTGCAACTCGAGGGCATGAAGTTGGAAATCGCTAGTA	1260
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Db	1261	ATGCGGAAACAGATGCGCGGGGTAAATACGTTCCCGGGCCCTGTACACACCGCCGCTCAC	1320
Qy	1321	ACCATGGAGCTGGTTCCTACCGACGACGNTGCGCTAACCTTCGGGGGGCAGCGGCCAC	1380
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Qy	1381	GGTAGGATCAGCGACTGGGGTGAAGTCGTAAACAAGGTAGCCGTAGGGGAACCTTCGCGGCTG	1440
Db	1381	GGTAGGATCAGCGACTGGGGTGAAGTCGTAAACAAGGTAGCCGTAGGGGAACCTTCGCGGCTG	1440
Qy	1441	GATCACCTCCTT	1452
Db	1441	GATCACCTCCTT	1452

RESULT 2
AAV22896

AAV22896
ID AAV22896 standard: DNA: 1452 BP.

XX
AC . AAV22896;XX
DT 28-JUL-1998 (first entry)

DE DNA encoding a colour improver.

XX Colour improver; E-396; FERM BP-4283; A-581-1; FERM BP-4671;
KW egg yolk colour; food; ds.
KW egg yolk colour; food; ds.

XX
OS E-396

XX PN JP09308481-A.

XX
PD
02-DEC-1997

23-MAY-1996: 96.TP-0128565

XX
PR 23-MAY-1996: 96.JP-0128565.

XX
PA (NTOC) NIPPON QTL CO LTD.

XX
DB WPT: 1998-070643/07

XX Colour Improver - useful to improve colour of foods and drinks

XX
PS
Nfisclosure: Page 13 of 14pp. Japanese

XX The present sequence encodes a novel colour improver and is isolated
CC

PA (NIOC) NIPPON OIL CO LTD.

XX Kiyota T, Takaki M, Tsubokura A, Yoneda H;

XX WPI; 1995-053688/08.

XX New bacteria which produce carotenoid pigments - used for the
 PT prodn. of astaxanthin, adonixanthin, beta-carotene, echinenone,
 PT canthaxanthin and zeaxanthin

XX Discløure; Page 20-21; 29pp; English.

CC This DNA sequence encodes a 16S rRNA isolated from a new genus of
 CC bacteria, designated E-396. This bacterium is capable of producing
 CC carotenoid pigments selected from astaxanthin, adonixanthin, beta-
 CC carotene, etc.. The carotenoid pigments can be produced in industrial
 CC quantities and used for feed additives.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 1451 BP; 353 A; 346 C; 460 G; 291 T; 1 other;

Query Match 99.1%; Score 1439; DB 16; Length 1451;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1451; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AGTTTGATCTCGGCTCAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
 DB 1 AGTTTGATCTCGGCTCAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
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 DB 61 GACCTTCGGGCTACGCGGACGCGGTGAGTAACGCGTGGGACGTCCTCTCTACGG 120
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 DB 421 ACCAGCAGAAGACCGCGGCTAACTCGTGCCAGCAGCCGCGGTAAATACGGAGGGGCT 480
 QY 481 AGCGTCTTCGGAATTAAGCTGAGGCTTAAGCCAGCAGTGGGAGCTGGAAGTCAAGGTG 540
 DB 481 AGCGTCTTCGGAATTAAGCTGAGGCTTAAGCCAGCAGTGGGAGCTGGAAGTCAAGGTG 540
 QY 541 AAATCCAGGCTCAACCTTGGAACTGCTTTGAAACTATATCAGTCTGGAGTTCGAGAGAG 600
 DB 541 AAATCCAGGCTCAACCTTGGAACTGCTTTGAAACTATATCAGTCTGGAGTTCGAGAGAG 600
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 DB 601 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAAACACCACTGGC 660
 QY 661 GAAAGCGGCTCAGTGGCTCGATATGACCGTGGAGTGGGAAAGCGTGGGGAGCAACAGG 720
 DB 661 GAAAGCGGCTCAGTGGCTCGATGACCGTGGAGTGGGAAAGCGTGGGGAGCAACAGG 720

RESULT 6

AAAX07384
 ID AAAX07384 standard; RNA; 1430 BP.
 XX
 AC AAAX07384;
 XX
 DT 07-JUN-1999 (first entry)
 XX
 DE Paracoccus marcusii 16S rRNA gene.
 XX
 KW Carotenoid; beta-carotene; echinenone; canthaxanthin;
 KW beta-cryptoxanthin; adonirubin; cis-adonixanthin;
 KW astaxanthin; zeaxanthin; pigment; ds.
 XX
 OS Paracoccus marcusii.
 XX
 PN W09906586-Al.
 XX
 PD 11-FEB-1999.
 XX

QY 721 ATTAGATACCTGTGTAGTCCACGCGTAAACGATGAATGCCAGACGTCGGCAAGCATGCT 780
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 QY 841 AACTCAAGGAATTGACGGGGCGGCGCACAGCGGTGAGCATGTGGTTTAAATTCGAAGC 900
 DB 841 AACTCAAGGAATTGACGGGGCGGCGCACAGCGGTGAGCATGTGGTTTAAATTCGAAGC 900
 QY 901 AACCGCAGAAACCTTACCAACCTTGACATGCGCAGACCGCTGGAGAGATTTCAGCTTCT 960
 DB 901 AACCGCAGAAACCTTACCAACCTTGACATGCGCAGACCGCTGGAGAGATTTCAGCTTCT 960
 QY 961 CGTAAGAGACCTGTCACACAGGTGTCGATGCGTGTGTCGAGTCTGTCGAGATGTTTC 1020
 DB 961 CGTAAGAGACCTGTCACACAGGTGTCGATGCGTGTGTCGAGTCTGTCGAGATGTTTC 1020
 QY 1021 GGTAAAGTCCGGCACAGGCGCAACCCACGTCCTTGTGTCAGCAATTCAGTTGGGAC 1080
 DB 1021 GGTAAAGTCCGGCACAGGCGCAACCCACGTCCTTGTGTCAGCAATTCAGTTGGGAC 1080
 QY 1081 TCTATGGAACCTGCCGATGATAAGTCGGAGGAAGGTGTGGATGAGTCAAGTCTCTCATGG 1140
 DB 1081 TCTATGGAACCTGCCGATGATAAGTCGGAGGAAGGTGTGGATGAGTCAAGTCTCTCATGG 1140
 QY 1141 GCCTTACGGTGGGCTACACAGTGTACAACTGCGAGGCGATGAACTTGGAAATCGGTAGTA 1200
 DB 1141 GCCTTACGGTGGGCTACACAGTGTACAACTGCGAGGCGATGAACTTGGAAATCGGTAGTA 1200
 QY 1201 AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATGAACTTGGAAATCGGTAGTA 1260
 DB 1201 AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATGAACTTGGAAATCGGTAGTA 1260
 QY 1261 ATCCGGAACAGCATGCCGCGTGAATACGTTCCCGGGCTTGTACACACCGCCGCTCAC 1320
 DB 1261 ATCCG-GAAGCATGCCGCGTGAATACGTTCCCGGGCTTGTACACACCGCCGCTCAC 1320
 QY 1321 ACCATGGAGTGGTTCTTACCGCAGCAGCGTACGCTAACCCTTCGGGGGCGAGCGGCCAC 1380
 DB 1321 ACCATGGAGTGGTTCTTACCGCAGCAGCGTACGCTAACCCTTCGGGGGCGAGCGGCCAC 1380
 QY 1381 GGTAGGATCAGGACTGGGGTGAAGTCGTAACAGGTAGCCGTAGGGAACCTGCGGCTG 1440
 DB 1381 GGTAGGATCAGGACTGGGGTGAAGTCGTAACAGGTAGCCGTAGGGAACCTGCGGCTG 1440
 QY 1441 GATCACTCTCTT 1452
 DB 1440 GATCACTCTCTT 1451

16-JUL-1998; 98WO-US14905.
 29-JUL-1997; 97US-0902618.
 (FRIE/) FRIEDMAN M M.
 (VISS) YISSUM RES & DEV CO.
 Harkar M, Hirschberg J;
 WPI; 1999-153810/13.
 New Paracoccus marcusii bacterium that produces and secretes
 carotenoid pigments - useful, as additives for animal feeds or human
 foods, in cosmetics and as pharmaceuticals
 Disclosure; Page 40-41; 55pp; English.
 This is the nucleotide sequence of the 16S ribosomal RNA gene of
 Paracoccus marcusii type strain DSM 11574 (also named Paracoccus
 strain WH1). The 16S rRNA gene can be used to identify this novel
 Paracoccus species. P. marcusii appeared as a single orange colony
 contaminating a nutrient agar plate. It produces and secretes
 carotenoids such as beta-carotene, echinenone, beta-cryptoxanthin,
 canthaxanthin, adonirubin, cis-adonixanthin, adonixanthin,
 astaxanthin and zeaxanthin in vesicles. A process for producing
 such carotenoids comprising culturing P. marcusii DSM 11574 in a
 nutrient medium including sources of carbon, nitrogen and inorganic
 substances, and recovering an individual carotenoid pigment or a
 mixture of carotenoid pigments from cells, vesicles and/or medium.
 The carotenoids are useful as additives for human foods or animal
 feeds (e.g. in salmonid fish farming) or cosmetics, and
 beta-carotene is used as a pharmaceutical. The new bacterium
 provides a ready source of carotenoids that are currently very
 expensive to synthesise or to extract from natural sources.
 Sequence 1430 BP; 349 A; 343 C; 456 G; 282 U; 0 other;
 Query Match 97.4%; Score 1414.8; DB 20; Length 1430;
 Best Local Similarity 80.0%; Pred. No. 0;
 Matches 1145; Conservative 282; Mismatches 3; Indels 1; Gaps 1;
 16 CAGACGACGCTGGCGGAGGCTTAACATCAAGTCGAGGAGACCTTCGGGTCTAG 75
 1 CAGACGACGCTGGCGGAGGCTTAACATCAAGTCGAGGAGACCTTCGGGTCTAG 60
 76 CGCGGACGCGGTGAGTAACGCGTGGGAACTGCGCTTCTACGGAATAGCCCGGAAA 135
 61 CGCGGACGCGGTGAGTAACGCGTGGGAACTGCGCTTCTACGGAATAGCCCGGAAA 120
 136 CTGGGAGTATACCGTATAGCCCTTTGGGGGAAAGATTATCGGAAAGATCGGCCG 195
 121 CUGGGAGUAUACCGUAUACCGCCUUGGGGAAAGUAUUGCGGAGGAUUGCGCCG 180
 196 CGTTGATAGTGTGTTGGGTATGTCGCCCAAGCGAGCTTACGTCATAGTGTGTT 255
 181 CGUUGAUAUAGUUGUUGGGGUAUUGGCCCAAGCGGAGGUAUUGCGGUAUUG 240
 256 GAGAGGATGATCAGCCACTGGGACTGAGACGCGGCCAGCTCTACGGGAGGACGA 315
 241 GAGAGGUAUAGCAGCACACUGGACUGACACGCGGCCAGACUCCUACGGGAGCA 300
 316 GTGGGATTTAGACAAATGGGGCAACCTGTATGATGATGATGATGATGATGATG 375
 301 GUGGGGAAUUAUAGAAUUGGGGCAACCCUGAUCUAGCCUAGCCGCGGUAUAG 360
 376 GCCTTAGGTTGTAAGCTTTTACGCTGGGAGATTAATACGCTACGACGAGGAGC 435
 361 GCCUUGAGGUAUAGGUAUAGGUAUAGGUAUAGGUAUAGGUAUAGGUAUAGG 420
 436 CCGGGTTAACTCCGTGCGACGCGCGGTAAATACGGAGGGGGGTACGCTGTTGCGGA 495
 421 CCGGGUAUACUCCGCGGACGCGCGGTAAATACGGAGGGGGGTACGCTGTTGCGGA 480

QY 496 TACTGGGCTAAAGCGACGCTAGCGAGCTGGAAGTCAGAGTGAATCCAGGGCTCA 555
 DB 481 UACUGGGCGUAAAGCGACGAGCGGAGCGUAGGAAAGUCAGAGGUAUCCAGGGCUCA 540
 QY 556 ACCTTGGAAGTCTTTTGAACATATCAGTCTGGAGTTTCGAGAGAGTGAATTCG 615
 DB 541 ACCUUGAAGCGUCCUUGAAGAAUACAGUCUGAGUUCGAGAGGUGAGUAGUCCG 600
 QY 616 AGTGTAGAGTGAATTCGTAGATATTCGAGGAAACACACAGTGGCGAGGCGCTACTG 675
 DB 601 AGUGAGAGGUGAAUUCGUAUUCGAGGAAACACACAGTGGCGAGGCGGCGUCACUG 660
 QY 676 GCTCGATACGACGCTGAGTGGGAAAGCTGGGAGCAACAGATTAAGATACCTCGT 735
 DB 661 GCGUAGUACUGACGUGAGGUGGAAAGCGGAGGAAACAGGUAUAGUACCCUGGU 720
 QY 736 AGTCCAGCGCTTAAACGATGAATCCAGAGCTCGGCAAGCATGCTTCTGGTGTACAC 795
 DB 721 AGUCCAGCGCGUAAACGAGUAGUAGCCAGACGCGGCAAGCAUGCUUCGUGUCACAC 780
 QY 796 TAACGGATTAAGCATTCGCGTGGGAGTACGCTGGCAGATTAATTAACACTCAAGGAAT 855
 DB 781 UACGGAUUAAGCAUUCGCGGAGGAGUACGCGGAGGAAUUAUUAUUAUUAUUAU 840
 QY 856 ACGGGGCGCGCACAGCGTGGGAGCATGCTGTTTAAATTCGAACGACGCGCAGACCT 915
 DB 841 ACGGGGCGCGCACAGCGGAGGAGCAUGGUGUUAUUAUUAUUAUUAUUAUUAUUA 900
 QY 916 ACCAACCTTGACATGCGAGGACGCTGGGAGATTCAGCTTCTCTAGAGACCTGCA 975
 DB 901 ACCAACCUUGACUAGCGAGGACGCGGAGGAGUAGUAGUAGUAGUAGUAGUAG 960
 QY 976 CACAGTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
 DB 961 CACAGGUGUGCAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 1020
 QY 1036 CGAGCGCAACCCAGCTCCCTAGTTCGAGCAATTCAGTGGGAACTCTATGGAACCTGC 1095
 DB 1021 CGAGCGCAACCCAGCTCCCTAGTTCGAGCAATTCAGTGGGAACTCTATGGAACCTGC 1079
 QY 1096 GATGATAAGTCGGAGGAGGCTGATGATGATGATGATGATGATGATGATGATGATG 1155
 DB 1080 GAUGAUAUAGCGAGGAGGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1139
 QY 1156 CTACACAGTGTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1215
 DB 1140 CUACACAGGUGUACAAUUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 1199
 QY 1216 GATTGTCTCTGCAACTCGAGGCGATGAAGTGAATCGCTAGTAAATCGCGGAAACAG 1275
 DB 1200 GAUUGUCCUUGCAACUUGGAGGCGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1259
 QY 1276 GCGCGGTGAATAGCTTCCGCGGCTTGTACACACCGCCGCTACACCATGGAGTTGGT 1335
 DB 1260 GCGCGGUAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1319
 QY 1336 TCTACCGAGCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1395
 DB 1320 UCUACCGAGCAGCUGGUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1379
 QY 1396 TGGGTGAAGTCTGAACAGTACCGCTAGGGAACCTGGGCTGGATCAC 1446
 DB 1380 UGGGGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1430
 RESULT 7
 ABL40152
 ID ABL40152 standard; DNA; 1426 BP.
 XX ABL40152;
 XX AC
 XX AC
 DT 18-MAY-2002 (first entry)
 XX

DE 16S ribosomal RNA from unknown organism A-581-1 DNA sequence SEQ ID NO:2.
XX
KW 16S ribosomal RNA; carotenoid pigment; microbial; carotenoid; pigment;
KW feed additive; food additive; pharmaceutical; gene; ss.
XX
OS Unidentified.
XX
PN W020196591-A1.
XX
PD 20-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-JP04874.
XX
PR 12-JUN-2000; 2000JP-0175124.
XX
PA (NIOC) NIPPON MITSUBISHI OIL CORP.
XX
PI Taubokura A, Mizuta H;
XX
DR WPI; 2002-122220/16.
XX
PT Microbial production of carotenoid pigments at varying ratios by
PT controlling concentration of oxygen dissolved in liquid culture medium,
PT useful in feed additives, food additives and pharmaceuticals
XX
PS Disclosure; Page 19; 23pp; Japanese.
XX
CC The present invention describes a microbial method for producing
CC carotenoid compounds at a specified, or varying, ratio by controlling
CC the concentration of oxygen dissolved in the liquid medium during
CC culture. The produced carotenoids are natural pigments, which are useful
CC in feed additives, food additives and pharmaceuticals. The ratio of the
CC carotenoid compounds obtained can be controlled by varying the
CC concentration of oxygen dissolved in liquid medium during culture.
CC The present sequence represents a 16S ribosomal RNA gene from an unknown
CC organism designated A-581-1 which is given in the exemplification of the
CC present invention.
XX
SQ Sequence 1426 BP; 349 A; 342 C; 451 G; 284 T; 0 other;

Query Match 95.0%; Score 1380; DB 24; Length 1426;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
QY 1 AGTTTGATCCTGGCTCAGAACGCTGGCGCAGGCTTAACATGCAAGTCGAGCGA 60
DB 4 AGTTTGATCCTGGCTCAGAACGCTGGCGCAGGCTTAACATGCAAGTCGAGCGA 63
QY 61 GACCTTCGGGTCTAGCGCGGACGGGTGAGTAAACGGTGGGACGTCCTCTACGG 120
DB 64 GACCTTCGGGTCTAGCGCGGACGGGTGAGTAAACGGTGGGACGTCCTCTACGG 123
QY 121 AATAGCCCGGAAACTGGGAGTAAATACCGTATACGCCCTTTGGGGAAAGATTATCGG 180
DB 124 AATAGCCCGGAAACTGGGAGTAAATACCGTATACGCCCTTTGGGGAAAGATTATCGG 183
QY 181 AGAAGGATCGGCCCGCGTTGGATTAGGTAGTTGGGTAAATGGCCCAAGCCGACG 240
DB 184 AGAAGGATCGGCCCGCGTTGGATTAGGTAGTTGGGTAAATGGCCCAAGCCGACG 243
QY 241 ATCCATAGTGTGTTGAGAGGATGATCACCACACTGGGACGTAGACAGCGGCCAGACTC 300
DB 244 ATCCATAGTGTGTTGAGAGGATGATCACCACACTGGGACGTAGACAGCGGCCAGACTC 303
QY 301 CTACGGGAGGACGAGTGGGGAACTTACACAAATGGGGCAACCTGTAGTCATAGCCATGCG 360
DB 304 CTACGGGAGGACGAGTGGGGAACTTACACAAATGGGGCAACCTGTAGTCATAGCCATGCG 363
QY 361 GCGTGAGTGATGAAGCCCTTAGGGTTGTAAGCTCTTTCAGCTGGGAAAGATTAATGACGGT 420
DB 364 GCGTGAGTGATGAAGCCCTTAGGGTTGTAAGCTCTTTCAGCTGGGAAAGATTAATGACGGT 423
QY 421 ACCAGCAGAAAGACCCCGGCTTAATCCGTGCGCAGACGCCCGGGTAAATACGAGGGGGCT 480

RESULT 8
ABL55950
ID ABL55950 standard; DNA; 1462 BP.
XX
AC ABL55950;

DB 424 ACCAGCAGAAAGAGCCCGGCTAACTCCGTGCCAGCAGCGCGGTAAATACGAGGAGGCT 483
QY 481 AGCGTTGTTCCGGAATTAATGCGGTAAAGCGACGAGTGGCGGACTGGAAGTCCAGAGGTG 540
DB 484 AGCGTTGTTCCGGAATTAATGCGGTAAAGCGACAGTGGCGGACTGGAAGTCCAGAGGTG 543
QY 541 AAATCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCACTGCTGGAGTTCGAGAGAG 600
DB 544 AAATCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCACTGCTGGAGTTCGAGAGAG 603
QY 601 GTGAGTGGAAATCCCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGACACACATGCG 660
DB 604 GTGAGTGGAAATCCCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGACACACATGCG 663
QY 661 GAAGGCGGCTCACTGCTCGATGACTGACGCTGAGGTGCGAAAGCGTGGGAGCAAAACAGG 720
DB 664 GAAGGCGGCTCACTGCTCGATGACTGACGCTGAGGTGCGAAAGCGTGGGAGCAAAACAGG 723
QY 721 ATTAGATACCTTGGTGTAGTCCACGCCGTAACGATGAATGCCAGACGTGCGCAAGCATGCT 780
DB 724 ATTAGATACCTTGGTGTAGTCCACGCCGTAACGATGAATGCCAGACGTGCGCAAGCATGCT 783
QY 781 TGTGCGGTGCACACCTAACGGATTAAAGCATTCGCCCTGGGGAGTACGGTCCGAAGTAA 840
DB 784 TGTGCGGTGCACACCTAACGGATTAAAGCATTCGCCCTGGGGAGTACGGTCCGAAGTAA 843
QY 841 AACTAAAGGAATTGACGGGGCCGCCAAGCGGTGGAGCATGTGGTTTAAATTCGAAGC 900
DB 844 AACTAAAGGAATTGACGGGGCCGCCAAGCGGTGGAGCATGTGGTTTAAATTCGAAGC 903
QY 901 AACGCGCAGAACCTTACCACCCCTTGACATGGCAGGACCGCTGGAGAGATTTCAGCTTCT 960
DB 904 AACGCGCAGAACCTTACCACCCCTTGACATGGCAGGACCGCTGGAGAGATTTCAGCTTCT 963
QY 961 CGTAAGACACTGACACAGGAGTGTGCTGATGGCTGTGCTGAGTCTGCTGAGATGCTTC 1020
DB 964 CGTAAGACACTGACACAGGAGTGTGCTGATGGCTGTGCTGAGTCTGCTGAGATGCTTC 1023
QY 1021 GGTAAAGTCCGCAAGCAGCGCAACCCAGTCCCTAGTTGGCCAGCAATTCAGTTGGGAAC 1080
DB 1024 GGTAAAGTCCGCAAGCAGCGCAACCCAGTCCCTAGTTGGCCAGC-ATTGAGTTGGGCAC 1082
QY 1081 TCTATGGAATGCCGATGATTAAGTCGGAGGAGGTGTGGATGACGTCAAGTCTCTCATGG 1140
DB 1083 TCTATGGAATGCCGATGATTAAGTCGGAGGAGGTGTGGATGACGTCAAGTCTCTCATGG 1142
QY 1141 GCGTTACGGGTTGGGCTACACAGTGTCTACAATGGTGTGACAGTGGGTTAATCCCCAAA 1200
DB 1143 CCGTTACGGGTTGGGCTACACAGTGTCTACAATGGTGTGACAGTGGGTTAATCCCCAAA 1202
QY 1201 AGCCATCTCAGTTGGGATTGTCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1260
DB 1203 AGCCATCTCAGTTGGGATTGTCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1262
QY 1261 ATCCGCGAAGACAGTATGCCCGGTGAATACGTTTCCCGGGCTTGTACACACCGCCGCTAC 1320
DB 1263 ATCCGCGAAGACAGTATGCCCGGTGAATACGTTTCCCGGGCTTGTACACACCGCCGCTAC 1322
QY 1321 ACCATGGGAGTGGTCTTACCCGACAGCAGTGGCTTAACC--TTCCGGGGGAGGCGGCC 1378
DB 1323 ACCATGGGAGTGGTCTTACCCGACAGCAGTGGCTTAACCCTTCGGGGAGGCGGCCGCC 1382
QY 1379 ACGGTAGGATACGACACTGGGTTGAAGTGTGAACAGGTAGCC 1421
DB 1383 ACGGTAGGATACGACACTGGGTTGAAGTGTGAACAGGTAGCC 1425

XX OS Paracoccus sp.
 XX PN JP10309190-A.
 XX PD 24-NOV-1998.
 XX PF 09-MAY-1997; 97JP-0136157.
 XX PR 09-MAY-1997; 97JP-0136157.
 XX PA (MITO) MITSUBISHI JUROGYO KK.
 XX PS WPI; 1999-073901/07.
 XX PT New selenic acid reducing microbe, Paracoccus genus - useful in
 PT removing selenium in waste water treatment
 XX Examples; Fig 5, 6; 13pp; Japanese.
 XX The invention relates to a selenic acid reducing microbe FERM BP-5662
 CC that belongs to Paracoccus genus. It has the ability of reducing 6-valent
 CC selenium (Se). Also provided is a method for waste water treatment
 CC comprising removing Se from waste water by reducing Se from 6-valent to
 CC 4-valent (optionally to an Se simple substance) by microbe (as above)
 CC treatment on the active sludge to separate the solid from the liquid.
 CC The microbe is useful in water treatment to remove (6-valent) selenium.
 CC The microbe is more efficient at removing 6-valent selenium than the
 CC prior art methods. The present sequence represents the nucleotide
 CC sequence of 16S rRNA that is used in the method of the invention.
 XX
 XX Sequence 1426 BP; 349 A; 316 C; 477 G; 284 T; 0 other;
 Query Match 85.7%; Score 1244.4; DB 20; Length 1426;
 Best Local Similarity 93.0%; Pred. No. 0;
 Matches 1325; Conservative 0; Mismatches 97; Indels 3; Gaps 2;
 QY 1 AGTTGATCTGCTCAGACGACGCTGGCGGAGCTTAACACATGCAAGTCGACGA 60
 DB 3 AGTTGATCTGCTCAGACGACGCTGGCGGAGCTTAACACATGCAAGTCGACGA 62
 QY 61 GACCTTCGGTCTAGCGGCGGAGGTGAGTACGCTGGGAGCGTCCCTTCTCTACGG 120
 DB 63 ACCCTTCGGGTTAGCGGCGGAGGTGAGTACGCTGGGAGCGTCCCTTCTCTACGG 122
 QY 121 AATAGCCCCGGGAACTGGGAGTAATACGTAATACGCTGGGAGGAAAGATTATCGG 180
 DB 123 AATAGCCCCGGGAACTGGGAGTAATACGTAATACGCTGGGAGGAAAGATTATCGG 182
 QY 181 AAGAGGATCGGCGGCTTGGATTAGTATGTTGGTGGGTAATGGGCCCAACGACG 240
 DB 183 CAAGGATTAGCGGCGGCTTGGATTAGTATGTTGGTGGGTAATGGGCCCAACGACG 242
 QY 241 ATCATAGCTGTTGAGAGGATGATCAGCCACATCGGAGTGGGAGACGCGCCAGACTC 300
 DB 243 ATCATAGCTGTTGAGAGGATGATCAGCCACATCGGAGTGGGAGACGCGCCAGACTC 302
 QY 301 CTACGGGAGCAGCTGGGAACTCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 360
 DB 303 CTACGGGAGCAGCTGGGAACTCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 362
 QY 361 CGGTGATGATGAAGGCTTAGGTTGTTAAGCTCTTTCAGCTGGGAGATATGACGGT 420
 DB 363 CGGTGATGATGAAGGCTTAGGTTGTTAAGCTCTTTCAGCTGGGAGATATGACGGT 422
 QY 421 ACCAGCAGAGAGCCCCGCTACTCCGTGCCAGCAGCGCGGTATATAGGAGGGGCT 480
 DB 423 ACCAGCAGAGAGCCCCGCTACTCCGTGCCAGCAGCGCGGTATATAGGAGGGGCT 482
 QY 481 AGCGTTTCTCGGAATTACTGGCGTAAGGCGCAGTGGGCGGAGTGGGAAGTTCAGAGGTG 540
 DB 483 AGCGTTTCTCGGAATTACTGGCGTAAGGCGCAGTGGGCGGAGTGGGAAGTTCAGAGGTG 542

QY 541 AATCCAGGGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTCGAGTTCGAGAGAG 600
 DB 543 AATCCAGGGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTCGAGTTCGAGAGAG 602
 QY 601 GTGAGTGAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAAACACCGATGCC 660
 DB 603 GTGAGTGAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAAACACCGATGCC 662
 QY 661 GAAGGGGCTCACTGGCTGCTACTGACGTGAGGTGCGAAGCGTGGGAGGAAACAGG 720
 DB 663 GAAGGGGCTCACTGGCTGCTACTGACGTGAGGTGCGAAGCGTGGGAGGAAACAGG 722
 QY 721 ATTAGATACCTTGTAGTCCACGCGCTAAACGATGAATGCCAGACGTCGGCAACATGCT 780
 DB 723 ATTAGATACCTTGTAGTCCACGCGCTAAACGATGAATGCCAGACGTCGGCAACATGCT 782
 QY 781 TGTGCGGTGCACACCTTAACGATTAACGATTCGCGCTGGGAGGTACGGTTCGCAAGATTAA 840
 DB 783 GTTCGGTGCACACCTTAACGATTAACGATTCGCGCTGGGAGGTACGGTTCGCAAGATTAA 842
 QY 841 AACTCAAGGAATTCAGCGGGGCGCCGACAGCGGTGGAGCATGTGTTTAAATTCGAGC 900
 DB 843 AATTCAAAGGAATTCAGCGGGGCGCCGACAGCGGTGGAGCATGTGTTTAAATTCGAGC 902
 QY 901 AACGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTACGCTTCT 960
 DB 903 AACGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTACGCTTCT 962
 QY 961 CGTAAGAGACCTGCACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 DB 963 GGTAAAGAGACCTGTGGACAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
 QY 1021 GGTAAAGTCCGCAACGAGCGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 1023 GGTAAAGTCCGCAACGAGCGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081
 QY 1081 TCTATGAAACTGCGGATGATTAAGTCGAGGAGGAGTGTGATGATGATGATGATGATGATGAT 1140
 DB 1082 TCTATGAAACTGCGGATGATTAAGTCGAGGAGGAGTGTGATGATGATGATGATGATGATGAT 1141
 QY 1141 GCCTTACGGTGGGCTACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 DB 1142 GCGTTAGGGTGGGCTACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201
 QY 1201 AGCATCTCAGTTCGGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 DB 1202 AGCATCTCAGTTCGGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
 QY 1261 ATCGCGAAGACAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 DB 1262 ATCGCGAAGACAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
 QY 1321 ACCATGGAGTGGTTCCTACCGGACGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1378
 DB 1322 ACCATGGAGTGGTTCCTACCGGACGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381
 QY 1379 ACGGTAGATCAGCAGTGGGTTGAAGTCTGTAACAGTAGCCGT 1423
 DB 1382 ACGGTAGCTCAGCAGTGGGTTGAAGTCTGTAACAGTAGCCGT 1426

RESULT 11

AAH48039
 ID AAH48039 standard; DNA; 1407 BP.

XX AC AAH48039;

XX AC
 DT 18-SEP-2001 (first entry)

XX DE Oligonucleotide SEQ ID 1.

XX KW Beta-hydroxybutyric acid; PHB; waste water treatment; ds.

OS Paracoccus kawasakienis.
XX JP2001145483-A.
XX 29-MAY-2001.
XX 19-NOV-1999; 99JP-0330419.
XX 19-NOV-1999; 99JP-0330419.
XX (BIOI-)*BIOINDUSTRY KYOKAI SH.
PA (AJIN) AJINOMOTO KK.
PA (KEI2-) KEIZAI SANGYOISHO SANGYO GIUTSU SOGO KEN.
XX WPI; 2001-387291/41.
DR A new microorganism Paracoccus kawasakienis is used for treatment of
XX waste water and production of beta-hydroxybutyric acid -
XX Disclosure; Page 4; 5pp; Japanese.
XX The present invention relates to a new beta-hydroxybutyric acid producing
CC microorganism Paracoccus kawasakienis (FERM P-17644, Bp-7059). The new
CC microorganism has properties of Paracoccus sp., is unable to grow in a
CC medium containing 0.3% or more of sodium chloride, unable to assimilate
CC potassium nitrate or glutamic acid, but is able to assimilate ammonium
CC sulphate as a nitrogen source. Also, the microorganism has urease or
CC lactase. The microorganism is able to assimilate xylose, mannitol, maltose or
CC sole carbon sources. The microorganism is useful for the production of
CC beta-hydroxybutyric acid (PHB) and treatment of waste water and reduction
CC of nitrate and removal of nitrogen in waste water. The present sequence
XX was used in the present invention.
XX SQ Sequence 1407 BP; 342 A; 341 C; 449 G; 275 T; 0 other;
Query Match 84.5%; Score 1227.2; DB 22; Length 1407;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 1319; Conservative 0; Mismatches 79; Indels 5; Gaps 4;
4 TTGATCTGCTCAGAACGAGCTGGCGCAGCTTAACACATGCAAGTCGAGCGAGAC 63
6 TTGATCTGCTCAGAACGAGCTGGCGCAGCTTAACACATGCAAGTCGAGCGCGCC 65
64 CTTGGGCTCAGCGCGGAGGTGAGTAACGGGTGGGAGCTGCGCTCTCTACGGAAT 123
66 CTTGGGCTCAGCGCGGAGGTGAGTAACGGGTGGGAGCTGCGCTCTCTACGGAAT 125
124 AGCCCGGGAACTGGGAGTAATACCGTATACGCCCTTTGGGGAAGATTTATCGGAGA 183
126 AGTCTCGGAACTGGGAGTAATACCGTATACGCCCTTTGGGGAAGATTTATCGGAGA 185
184 AGGATCGGCGCGGTTGGATTAGTGTGGTGGTAAAGCTTTTCAGCTGGGGAAGATTAATGACGTAC 243
186 AGATCGGCGCGGTTGGATTAGTGTGGTGGTAAAGCTTTTCAGCTGGGGAAGATTAATGACGTAC 245
244 CATAGTGTGTTGAGAGGATGATACGCCACTGGGAGCTGAGACAGCGGCCAGACTCCTTA 303
246 CATAGTGTGTTGAGAGGATGATACGCCACTGGGAGCTGAGACAGCGGCCAGACTCCTTA 305
304 CGGAGGACGACGTGGGATCTTATACATATGGGGCAACCCCTGATCTAGCCATGCCGCG 363
306 CGGAGGACGACGTGGGATCTTATACATATGGGGCAACCCCTGATCTAGCCATGCCGCG 365
364 TGAGTATGAGGCTTTAGGTTGTTAAAGCTTTTCAGCTGGGGAAGATTAATGACGTAC 423
366 TGAGGATGAGGCTTTAGGTTGTTAAAGCTTTTCAGCTGGGGAAGATTAATGACGTAC 425
424 AGCAGAAGAGCCCGGCTTAATCCGTGCCAGCAGCGCGGTAAATACGGAGGGGGGTAGC 483
426 AGCAGAAGAGCCCGGCTTAATCCGTGCCAGCAGCGCGGTAAATACGGAGGGGGGTAGC 485
484 GTTGTTCGGGAATTACTTGGGCGTAAGCGGACGTAGCGGACTGGGAAAGTCAGAGGTGAAA 543

486 GTTGTTCGGGAATTACTTGGGCGTAAAGCGCACGTAGCGGATCAGAAAGTCAGAGGTGAAA 545
544 TCCAGGGCTCAACCTTGGAACTGCCCTTTGAAACTATCATCTGGAAGTTCGAGAGAGGTG 603
546 TCCAGGGCTCAACCTTGGAACTGCCCTTTGAAACTATCATCTGGAAGTTCGAGAGAGGTG 605
604 AGTGAATTCGAGTGTAGAGTGAATTCGATATTCGAGAGTTCGAGAGAGGTG 663
606 AGTGAATTCGAGTGTAGAGTGAATTCGATATTCGAGAGTTCGAGAGAGGTG 665
664 GCGGCTCACTGCTGATACCTGAGTGAATTCGATATTCGAGAGTTCGAGAGAGGTG 723
666 GCGGCTCACTGCTGATACCTGAGTGAATTCGATATTCGAGAGTTCGAGAGAGGTG 725
724 AGATACCTGCTGATACCTGAGTGAATTCGATATTCGAGAGTTCGAGAGAGGTG 783
726 AGATACCTGCTGATACCTGAGTGAATTCGATATTCGAGAGTTCGAGAGAGGTG 785
784 CGGTGCACACTTAACGATTAAGCATTCGCTGGGAGTACGGTTCGAGAGTTCGAGAGAG 843
786 CGGTGCACACTTAACGATTAAGCATTCGCTGGGAGTACGGTTCGAGAGTTCGAGAGAG 845
844 TCAAGGAATTCAGGG 903
846 TCAAGGAATTCAGGG 905
904 GCGAGAACCTTACCAACCTTGCATGTCGAGAGTTCGAGAGTTCGAGAGTTCGAGAG 962
906 GCGAGAACCTTACCAACCTTGCATGTCGAGAGTTCGAGAGTTCGAGAGTTCGAGAG 965
963 TAAGAGA-CCTGTCACAGAGTGTGTCGTCGAGTTCGTCGTCGTCGTCGTCGTCGTCG 1021
966 TAAGAGACCTTCGACAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1025
1022 GTTAAGTCGCGGAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1081
1026 GTTAAGTCGCGGAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1084
1082 CTATGAAACTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1141
1085 TTAGGAGAACTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1144
1142 CTTAGCGGTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCG 1201
1145 CTTAGCGGTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCG 1204
1202 GCGATCTCAGTTCGAGTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTC 1261
1205 GCGATCTCAGTTCGAGTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTC 1264
1262 TCAGGAGAACAGCATTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTCG 1321
1265 TCAGGAGAACAGCATTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTCG 1324
1322 CCATGGAGTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCG 1379
1325 CCATGGAGTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCG 1384
1380 CGGTAGGATTCAGGAGTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTC 1402
1385 CGGTAGGATTCAGGAGTTCGCGGATGATAAGTCGAGGAGTTCGAGTTCGAGTTCGAGTTC 1407
RESULT 12
AAC87598
ID AAC87598 standard; DNA; 1430 BP.
XX
XX AAC87598;
XX
XX 16-MAR-2001 (first entry)
XX
XX Bacterium SH134-8 (FERM P-17192) 16S rDNA.

XX SH134-8; FERM P-17192; Gram negative; aerobic; heterotrophic;
KW hydroxylaminodisulphonate acid; HADS decomposition; 16S rDNA; ds.
XX Bacteria.
OS JP2000287678-A.
XX 17-OCT-2000.
XX 09-APR-1999; 99JP-0102575.
XX 09-APR-1999; 99JP-0102575.
XX (MITO) MITSUBISHI JUKOYO KK.
XX WPI; 2001-127271/14.
DR A microbe decomposing a nitrogen-containing sulfur compound -
XX Disclosure; Page 4; 5pp; Japanese.
XX The invention relates to a novel bacterium, designated SH134-8 in
CC the specification, which is able to decompose the nitrogen-containing
CC sulphur compound HADS (hydroxylaminodisulfonic acid). Bacterium SH134-8
CC (FERM P-17192) is an aerobic heterotrophic Gram-negative bacterium which
CC is non-motile and has no sugar-assimilating ability. Bacterium SH134-8
CC can be used for decomposing a nitrogen-containing sulphur compound such
CC as HADS in a cost-effective manner e.g., for environmental
CC decontamination. The present sequence represents DNA encoding 16S
CC ribosomal RNA (16S rDNA) from bacterium SH134-8.
XX Sequence 1430 BP; 342 A; 351 C; 456 G; 281 T; 0 other;
SQ
Query Match 83.0%; Score 1205.4; DB 22; Length 1430;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 107; Indels 5; Gaps 4;
QY 1 AGTTTGATCTCGTCTAGACGACGCTGGGGGAGGCTTAACACATGCAAGTCGAGCGA 60
DB 4 AGTTTGATCTCGTCTAGACGACGCTGGGGGAGGCTTAACACATGCAAGTCGAGCGC 63
QY 61 GACCTTCGGGTCTACGGCGGACGGGTGAGTAACGCGTGGGAACGCTTCTCTACGG 120
DB 64 GCCCTTCGGGTGACGGCGGACGGGTGAGTAACGCGTGGGAACGCTTCTCTACGG 123
QY 121 AATAGCCCCGGGAACTGGGAGTAATACCGTATACGCCCTTTGGGGGAAAGATTATCGG 180
DB 124 AATAGCCACTGGAAACGGTGAGTAATACCGCATACGCCCTTCGGGGGAAAGATTATCGG 183
QY 181 AGAAGGATCGGCCCGCTTGGATTAGTATGTTGGGTAAATGGCCCAACCAAGCCGACG 240
DB 184 AGGAGGATCGGCCCGCTTGGATTAGTATGTTGGGTAAATGGCCCAACCAAGCCGACG 243
QY 241 ATCCATAdCTGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC 300
DB 244 ATCCATAGCTGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC 303
QY 301 CTACGGGAGGACAGTGGGAACTCTTAGACAATGGGGGCAACCCCTGATCTAGCCATGCC 360
DB 304 CTACGGGAGGACAGTGGGAACTCTTAGACAATGGGGGCAACCCCTGATCTAGCCATGCC 363
QY 361 CGGTGAGTATGAAGGCTTAGGTTTAAAGCTCTTTCAGCTGGGAGGATAAATGACGGT 420
DB 364 CGGTGAGTATGAAGGCTTAGGTTTAAAGCTCTTTCAGCTGGGAGGATAAATGACAGT 423
QY 421 ACCAGCAGAGAAGCCCGGCTACTCGTCCAGCAGCCCGGCTTAATACGGAGGGGCT 480
DB 424 AGCAGGTAAGAAACCCCGGCTAACTCCGTCCAGCAGCCCGGCTTAATACGGAGGGGCT 483
QY 481 AGCGTGTTCGGAATTAATCTGGGCGTAAAGCAGCAGCTAGGCGGACTGGAAAGTCAGAGGTG 540
DB 484 AGCGTGTTCGGAATTAATCTGGGCGTAAAGCAGCAGCTAGGCGGACTGGAAAGTGGGGGTG 543

QY 541 AATCCAGGCTCAACCTTGAAGTCTGCTTTTGAAGTATCAGTCTGGAGTTCGAGAGG 600
DB 544 AATCCAGGCTCAACCTTGAAGTCTGCTTTTGAAGTATCAGTCTGGAGTTCGAGAGG 603
QY 601 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGAGAACACCAAGTGC 660
DB 604 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGAGAACACCAAGTGC 663
QY 661 GAAGCGGCTCAGTGGTCTGATAGTGGTGAAGTGGTGAAGTGGGAGCAACAGG 720
DB 664 GAAGCGGCTCAGTGGTCTGATAGTGGTGAAGTGGTGAAGTGGGAGCAACAGG 723
QY 721 ATTAGATACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 780
DB 724 ATTAGATACCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 783
QY 781 TGTCGGTGTACACCTAACGATTAAGCATTCGCGCTGGGAGTACGCTGCGCAAGTAA 840
DB 784 TGTCGGTGTACACCTAACGATTAAGCATTCGCGCTGGGAGTACGCTGCGCAAGTAA 843
QY 841 AACTCAAGGAATTCAGCGGCGCGCAACAGCGTGGAGTATGCTGCTTAAATTCGAAGC 900
DB 844 AACTCAAGGAATTCAGCGGCGCGCAACAGCGTGGAGTATGCTGCTTAAATTCGAAGC 903
QY 901 AACCGCGAGAACCTTACCAACCTTGACATGG-CAGGACCGCTGGAGAGATTCAGCTTTC 959
DB 904 AACCGCGAGAACCTTACCAACCTTGACATGGATATCGCGGACCAAGAGATGCTTTC 963
QY 960 TCGTAAG-AGACCTGCACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1018
DB 964 AGTTCGGTGTGATATCACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
QY 1019 TCGGTTAAGTCCGCAAGGAGCGCAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077
DB 1024 TCGGTTAAGTCCGCAAGGAGCGCAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
QY 1078 AACTCTATGGAACCTGCGGATGATGAAGTGGGAGGAGTGTGGATGACGTCAGTCAAGTCTCA 1137
DB 1084 CACTCTGGAACCTGCGGATGATGAAGGAGGAGGAGTGTGGATGACGTCAGTCAAGTCTCA 1143
QY 1138 TGGGCTTACGGTGGGCTACACACGCTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
DB 1144 TGGGCTTACGGTGGGCTACACACGCTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1203
QY 1198 AAAAGCCATCTCAGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
DB 1204 AAAAGCCATCTCAGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263
QY 1258 GTAATCGGGAACAGCATGCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
DB 1264 GTAATCGGGAACAGCATGCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1323
QY 1318 CACACCATGGAGTGGTTCCTACCGGAGGAGTGGTTCGCTAACCC--TTGCGGGGAGGAGCGG 1375
DB 1324 CACACCATGGAGTGGTTCCTACCGGAGGAGTGGTTCGCTAACCCCTTACCGGAGGAGCGG 1383
QY 1376 GCCACGGTATGATCAGCAGTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421
DB 1384 ACCACGGTATGCTCAGCAGTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1429

RESULT 13

ABL40356

ID ABL40356 standard; DNA; 1430 BP.

XX ABL40356;

AC ABL40356;

XX 01-JUL-2002 (first entry)

XX Polynucleotide sequence specific to a HADS decomposing microbe.

XX HADS; decomposing; ds.

KW HADS; decomposing; ds.

[illegible]

[illegible]

Search completed: July 28, 2003, 09:25:02
Job time : 355 secs

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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 09:18:53 ; Search time 111 seconds
(without alignments)
5773.769 Million cell updates/sec

Title: US-10-049-228-1
Perfect score: 1452
Sequence: 1 agtttgatcctggctcagaa.....tcggctgtgattcactcctt 1452

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1451	99.9	1452	1	US-08-276-943-1
2	1451	99.9	1452	2	US-08-716-841-1
3	1414.8	97.4	1430	2	US-08-902-518A-1
4	1227.2	84.5	1407	4	US-09-517-744B-1
5	1198.6	82.5	1419	4	US-09-565-063-2
6	1086.4	74.8	1502	3	US-09-187-946-2
7	1036.4	71.4	1415	2	US-08-632-470-52
8	987.4	68.0	1556	3	US-08-995-960-1
9	980.2	67.5	1508	2	US-08-632-470-44
10	973.6	67.1	1436	4	US-09-347-001-2
11	960.4	66.1	1438	4	US-09-347-001-1
12	944.2	65.0	1494	2	US-08-632-470-49
13	944	65.0	1440	2	US-08-632-470-33
14	944	65.0	1440	2	US-08-632-470-36
15	942.4	64.9	1440	2	US-08-632-470-35
16	942	64.9	1438	2	US-08-632-470-24
17	940.8	64.8	1440	2	US-08-632-470-23
18	940.8	64.8	1440	2	US-08-632-470-29
19	940.8	64.8	1458	2	US-08-632-470-45
20	940	64.7	1436	2	US-08-632-470-34
21	939.2	64.7	1440	2	US-08-632-470-26
22	939.2	64.7	1440	2	US-08-632-470-28
23	938.2	64.6	1441	2	US-08-632-470-38
24	936	64.5	1440	2	US-08-632-470-41
25	934.4	64.4	1440	2	US-08-632-470-37
26	934.4	64.4	1440	2	US-08-632-470-39
27	932.8	64.2	1440	2	US-08-632-470-46

28	932.4	64.2	1442	2	US-08-632-470-30	Sequence 30, Appl
29	931.4	64.1	1439	2	US-08-632-470-31	Sequence 31, Appl
30	931.2	64.1	1432	2	US-08-632-470-25	Sequence 25, Appl
31	930	64.0	1569	2	US-08-632-470-47	Sequence 47, Appl
32	929.6	64.0	1440	2	US-08-632-470-43	Sequence 43, Appl
33	926.2	63.8	1427	2	US-08-632-470-27	Sequence 27, Appl
34	920.4	63.4	1432	2	US-08-632-470-32	Sequence 32, Appl
35	914.2	63.0	1498	2	US-08-632-470-51	Sequence 51, Appl
36	913.8	62.9	1439	3	US-08-632-470-42	Sequence 42, Appl
37	904.8	62.3	1208	3	US-09-187-946-1	Sequence 1, Appl
38	904	62.3	1408	2	US-08-632-470-40	Sequence 40, Appl
39	899.2	61.9	1483	3	US-08-953-171-7	Sequence 7, Appl
40	863.8	59.5	1435	2	US-08-632-470-48	Sequence 48, Appl
41	861.8	59.4	1501	4	US-09-793-920A-1	Sequence 1, Appl
42	861.8	59.4	1501	4	US-09-821-016-5	Sequence 5, Appl
43	861.8	59.4	1501	4	US-09-745-476-1	Sequence 1, Appl
44	861.8	59.4	1501	4	US-09-748-205-1	Sequence 1, Appl
45	857.6	59.1	1540	4	US-09-228-184-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-276-943-1
; Sequence 1, Application US/08276943
; Patent No. 5607839
; GENERAL INFORMATION:
; APPLICANT: Tsubokura, Akira
; APPLICANT: Yoneda, Hisashi
; APPLICANT: Takaki, Mikihiro
; APPLICANT: Kiyota, Takashi
; TITLE OF INVENTION: BACTERIA BELONGING TO NEW GENUS AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CAROTENOIDS USING SAME
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed & Berry
; SURETY: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,943
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 700085.407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to rRNA
US-08-276-943-1

Query Match 99.9%; Score 1451; DB 1; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTTTGATCTGCTCAGAACGCTGCGGAGCGCTTAACACATGCAAGTCGAGCGA 60

1 AGTTTGGCTCTGCTCAGAACGACGCTGGCGGACGCTTAACACATGCAAGTCGACGCA 60
61 GACCTTCGGGTCTAGCGCGGAGCGGTGAGTACCGGTGGGACGCTGCGCTTCTCTACGG 120
61 GACCTTCGGGTCTAGCGCGGAGCGGTGAGTACCGGTGGGACGCTGCGCTTCTCTACGG 120
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241 ATCCATAGCTGTTTTCAGAGGATGATCAGCCACACTGGGACCTGAGACACGCGCCAGACTC 300
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301 CTACGGGAGCAGCAGTGGGGAATCTTACAGCAATGGGGCAACCCCTGATCTAGCCATGCC 360
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1201 AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTA 1260
1261 ATCGGGGAACAGCATGCGCGGTGAATAGTTCGCCGGCTGTACACACCGCGCTCAC 1320
1261 ATCGGGGAACAGCATGCGCGGTGAATAGTTCGCCGGCTGTACACACCGCGCTCAC 1320
1321 ACCATGGGAGTGGTCTTACCCGACGACGNTGGCTAACTTCGGGGGCGAGCGGCCAC 1380
1321 ACCATGGGAGTGGTCTTACCCGACGACGNTGGCTAACTTCGGGGGCGAGCGGCCAC 1380
1381 GGTAGATCAGGACTGGGCTGAAGTCGTAACAAAGTAGCGGTAGGGGAACCTGCGGCTG 1440
1381 GGTAGATCAGGACTGGGCTGAAGTCGTAACAAAGTAGCGGTAGGGGAACCTGCGGCTG 1440
1441 GATCACCCTCTT 1452
1441 GATCACCCTCTT 1452

RESULT 2
US-08-716-841-1
; Sequence 1, Application US/08716841
; Patent No. 5858761
; GENERAL INFORMATION:
; APPLICANT: Tsubokura, Akira
; APPLICANT: Yoneda, Hisashi
; APPLICANT: Takaki, Mikihiro
; APPLICANT: Kiyota, Takashi
; TITLE OF INVENTION: BACTERIA BELONGING TO NEW GENUS AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CAROTENOIDS USING SAME
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed & Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,841
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,943
; FILING DATE: 19-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 700085.407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to rRNA

QY	1021	GGTTAAGTCGGGCAACGAGCGCAACCCAGCTCCCTAGTTGCCAGCAATTCAGTTGGGAAC	1080
Db	1021	GGTTAAGTCGGGCAACGAGCGCAACCCAGCTCCCTAGTTGCCAGCAATTCAGTTGGGAAC	1080
QY	1081	TCFATGAAACTCCCGATGATAAGTCGGAGGAAAGTGTGGATCAGCTCAAGTCTCATGG	1140
Db	1081	TCFATGAAACTCCCGATGATAAGTCGGAGGAAAGTGTGGATCAGCTCAAGTCTCATGG	1140
QY	1141	GCCTTACGGGTTGGGCTACACACGTCGCTACAATGGTGGTGACAGTGGGTTAATCCCAAA	1200
Db	1141	GCCTTACGGGTTGGGCTACACACGTCGCTACAATGGTGGTGACAGTGGGTTAATCCCAAA	1200
QY	1201	AGCCATCTCAGTTCGGATGTTCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA	1260
Db	1201	AGCCATCTCAGTTCGGATGTTCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA	1260
QY	1261	ATCGCGGAACAGCATGCCGGGTGAATACGTTCCCGGGCCTTGACACACCGCCGCTCAC	1320
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QY	1321	ACCATGGGAGTTGGTCTTACCCGACGACGNTGGCGCTAAACCTTCGGGGGGCAGGCGGCCAC	1380
Db	1321	ACCATGGGAGTTGGTCTTACCCGACGACGNTGGCGCTAAACCTTCGGGGGGCAGGCGGCCAC	1380
QY	1381	GGTAGATCAGCAGCTGGGTTGAAGTCGTTAAACAAAGGTAGCCGTAGGGGAACCTGCGGCTG	1440
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QY	1441	GATCACCTCCTT 1452	
Db	1441	GATCACCTCCTT 1452	

RESULT 3
 US-08-902-518A-1
 ; Sequence 1, Application US/08902518A
 ; Patent No. 5935808
 ; GENERAL INFORMATION:
 ; APPLICANT: Joseph Hirschberg and Mark Harker
 ; TITLE OF INVENTION: NOVEL CAROTENOID-PRODUCING BACTERIAL
 ; TITLE OF INVENTION: SPECIES AND PROCESS FOR PRODUCTION
 ; TITLE OF INVENTION: OF CAROTENOIDS USING SAME
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
 ; STREET: 2940 Birchtree lane
 ; CITY: Silver Spring
 ; STATE: Maryland
 ; COUNTRY: United States of America
 ; ZIP: 20906
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
 ; COMPUTER: Twinhead* Slimnote-890TX
 ; OPERATING SYSTEM: MS DOS version 6.2.
 ; OPERATING SYSTEM: Windows version 3.11
 ; SOFTWARE: Word for Windows version 2.0 converted to
 ; SOFTWARE: an ASCII file
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/902,518A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Friedman, Mark M.
 ; REGISTRATION NUMBER: 33,883.
 ; REFERENCE/DOCKET NUMBER: 325/20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 972-3-5625553

TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-902-518A-1

Query Match 97.4%; Score 1414.8; DB 2; Length 1430;
Best Local Similarity 80.0%; Pred. No. 0;
Matches 1145; Conservative 282; Mismatches 3; Indels 1; Gaps 1;
QY 16 CAGAACGCTGCGCGCAGGCTTAACATGCAAGTCGAGCAGAGACCTTCGGGTCTAG 75
DB 1 CAGAACGCTGCGCGCAGGCTTAACATGCAAGTCGAGCAGAGACCTTCGGGTCTAG 60
QY 76 CGCGGACGGGTGAGTAACGCTGCGGACGCTGCTCTACGGAATAGCCCGGGA 135
DB 61 CGCGGACGGGTGAGTAACGCTGCGGACGCTGCTCTACGGAATAGCCCGGGA 120
QY 136 CTGGAGTAATACCGTATACCCCTTTGGGGAAAGATTATTCGAGAGAGATGGCCCG 195
DB 121 CUGGAGTAATACCGTATACCCCTTTGGGGAAAGATTATTCGAGAGAGATGGCCCG 180
QY 196 CGTGGATTAGTAGTGGTGGTAAATGGCCCAACAGCCGACATCCATAGCTGTTT 255
DB 181 CGTGGATTAGTAGTGGTGGTAAATGGCCCAACAGCCGACATCCATAGCTGTTT 240
QY 256 GAGAGATGATCAGCACACCTGAGTACGACGCGCCACACTCTACGAGGAGCAGCA 315
DB 241 GAGAGATGATCAGCACACCTGAGTACGACGCGCCACACTCTACGAGGAGCAGCA 300
QY 316 GTGGGATCTTACGATATGGGGCAACCTGATCTAGCCATGCGGCTGAGTATGAG 375
DB 301 GUGGGAAUCUAGCAAAUGGGGCAACCCUGAUCAGCAAGCCGCGUGAGUGAAG 360
QY 376 CCCTTAGGTTGTAAGCTCTTTCAGCTGGGAAGTAATGACCGTACAGCAGAGAGC 435
DB 361 CCCTTAGGTTGTAAGCTCTTTCAGCTGGGAAGTAATGACCGTACAGCAGAGAGC 420
QY 436 CCGGCTAACCTCCGTCAGCAGCGCGGTAATACGAGGCGGTACGTTGTTCCGAT 495
DB 421 CCGGCTAACCTCCGTCAGCAGCGCGGTAATACGAGGCGGTACGTTGTTCCGAT 480
QY 496 TACTGGGCTAAAGCGACGTAGCGGACTGGAAGTCAGAGTGAATCCAGGGTCA 555
DB 481 UACUGGCGUAAAGCGACGTAGCGGACTGGAAGTCAGAGTGAATCCAGGGTCA 540
QY 556 ACCTTGAACCTGCTTGAACACTATCATCTGAGTGGAGTTCGAGAGAGTGGAAATCCG 615
DB 541 ACCUUGGAACUGCCUUGAAGAACUACUCUGGAGUUCGAGAGAGUGAGUGGAAUCCG 600
QY 616 AGTGTAGAGTGAATTCGTAGATATTCGAGGAGACACACTGTCGAGGCGGTCACTG 675
DB 601 AGTGTAGAGTGAATTCGTAGATATTCGAGGAGACACACTGTCGAGGCGGTCACTG 660
QY 676 GCTCATACTGACCTGAGTGGCGAAACGCTGGGAGCAACAGGATTAGATACCTCGT 735
DB 661 GCUCAUACGACGCGUGAGGCGGAAAGCGUGGAGCAACAGGAAUAGAUACCCUGGU 720
QY 736 AGTCCAGCCGTAACAGTGAATGCCAGAGCTGCGCAAGCATGTTCTCGGTGTCACAC 795
DB 721 AGUCCAGCCGTAACAGTGAATGCCAGAGCTGCGCAAGCATGTTCTCGGTGTCACAC 780
QY 796 TAACGATTATAGCATTCGCGCTGGGAGTACGCTGCGCAAGTAAACTCAAGGAATTG 855
DB 781 TAACGATTATAGCATTCGCGCTGGGAGTACGCTGCGCAAGTAAACTCAAGGAATTG 840
QY 856 ACGGGGCCGCCACAAAGCGGTGGAGCATGTGTTTAAATCGAAGCAACCGCAGCAACTT 915
DB 841 ACGGGGCCGCCACAAAGCGGTGGAGCATGTGTTTAAATCGAAGCAACCGCAGCAACTT 900

QY 916 ACCAACCTTGCATGATGCGAGACCGCTGGAGAGATTTCAGTTTCGTGAAGAGACTCA 975
DB 901 ACCAACCTTGCATGATGCGAGACCGCTGGAGAGATTTCAGTTTCGTGAAGAGACTCA 960
QY 976 CACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
DB 961 CACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1036 CGAGCGCAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
DB 1021 CGAGCGCAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1079
QY 1096 GATGATAGTTCGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1155
DB 1080 GAUGAUAAGTCGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1139
QY 1156 CTACACAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1215
DB 1140 CTACACAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1199
QY 1216 GATTGCTGCTGCAACTCGAGGCGATGAATGGAATGGAATGGAATGGAATGGAATGGAATG 1275
DB 1200 GAUUGUCCUGCAACUCGAGGCGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUG 1259
QY 1276 GCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1335
DB 1260 GCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1319
QY 1336 TCTACCGGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1395
DB 1320 TCTACCGGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1379
QY 1396 TGGGCTGAAGTCGTAACAAAGTACGCTGAGGGAACCTGCGGCTGATCAAC 1446
DB 1380 UGGGUGAAGUCGUACAAGGAGCCGUGAGGGAACCCUGGCGUGGAGUAC 1430

RESULT 4
US-09-517-744B-1
; Sequence 1, Application US/09517744B
; Patent No. 6391576
; GENERAL INFORMATION:
; APPLICANT: TSUCHIDA, Takayasu
; APPLICANT: MANOME, Akira
; APPLICANT: KURANE, Ryuchiro
; TITLE OF INVENTION: METHOD FOR ISOLATING A MICROBE
; FILE REFERENCE: 0010-1089-0X
; CURRENT APPLICATION NUMBER: US/09/517,744B
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Paracoccus kawasakiiensis
US-09-517-744B-1

Query Match 84.5%; Score 1227.2; DB 4; Length 1407;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 1319; Conservative 0; Mismatches 79; Indels 5; Gaps 4;
QY 4 TTGATCTGCTCAGAACGACGCTGGCGGAGCTTAAACATGCAAGTTCGAGCAGAC 63
DB 6 TTGATCTGCTCAGAACGACGCTGGCGGAGCTTAAACATGCAAGTTCGAGCAGAC 65
QY 64 CTTCGGGTGAGCGCGGAGTAACTACCGTATACCGCTTTCCTCTACGGAAT 123
DB 66 CTTCGGGTGAGCGCGGAGTAACTACCGTATACCGCTTTCCTCTACGGAAT 125
QY 124 AGCCCCGGGAACTGGGAGTAACTACCGTATACCGCTTTCCTCTACGGAAT 183
DB 126 AGTCTGGGAACTGGGAGTAACTACCGTATACCGCTTTCCTCTACGGAAT 185

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184 AGGATCGGCCCGCTTGGATTAGTGTGGGTAAATGGCGTAAATGGCCACCAAGCGGAGATC 243
186 AGGATCGGCCCGCTTGGATTAGTGTGGGTAAATGGCGTAAATGGCCACCAAGCGGAGATC 245
244 CATAGCTGTTTGGAGAGGATGATAGCCACACTGGGACTGAGACAGCGGCCAGACTCCCTA 303
246 CATAGCTGTTTGGAGAGGATGATAGCCACACTGGGACTGAGACAGCGGCCAGACTCCCTA 305
304 CGGGAGGACAGAGTGGGGAATCTTAGACAATGGGGCAACCTGTATGATGACCATGCGCGG 363
306 CGGGAGGACAGAGTGGGGAATCTTAGACAATGGGGCAACCTGTATGATGACCATGCGCGG 365
364 TGAGTGATGAAGCGCTTAGGTTGTAAGCTCTTTCAGCTGGGAAGATAATGAGGTACC 423
366 TGAGCGATGAAGCGCTTAGGTTGTAAGCTCTTTCAGCTGGGAAGATAATGAGGTACC 425
424 AGCAGAAGAGCCCGGCTTAACCTCGGTGCACAGCGCGGTAATACGGAGGGGGTAGC 483
426 AGCAGAAGAGCCCGGCTTAACCTCGGTGCACAGCGCGGTAATACGGAGGGGGTAGC 485
484 GTTGTTCGAATTAATGCGCGTAAAGCGCACGTAGGCGGACTGGGAAGTCAAGAGTGA 543
486 GTTGTTCGAATTAATGCGCGTAAAGCGCACGTAGGCGGACTGAGAAAGTCAAGAGTGA 545
544 TCCAGGGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTGGAGTTCGAGAGAGTG 603
546 TCCAGGGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTGGAGTTCGAGAGAGTG 605
604 AGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGA 663
606 AGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGA 665
664 GCGGCTCACTGGCTGATCTGACGCTGAGTGCAGGAGCGTGGGAGCAACACAGGAT 723
666 GCGGCTCACTGGCTGATCTGACGCTGAGTGCAGGAGCGTGGGAGCAACACAGGAT 725
724 AGATACCTTGGTGTAGTCCAGCGCTAAACGATGATGATGATGATGATGATGATGAT 783
726 AGATACCTTGGTGTAGTCCAGCGCTAAACGATGATGATGATGATGATGATGATGAT 785
784 CGGTGTACACCTTAACGATTAAGCATTCGCTCGGGGAGTACGGTGCAGAAATTAAC 843
786 CGGTGTACACCTTAACGATTAAGCATTCGCTCGGGGAGTACGGTGCAGAAATTAAC 845
844 TCAAGGAATTAACGAGGCGCCGACACAGCGTGGAGCATGTGTTTAAATTCGAAGCAAC 903
846 TCAAGGAATTAACGAGGCGCCGACACAGCGTGGAGCATGTGTTTAAATTCGAAGCAAC 905
904 GCGCAGAACCTTACCAACCTTGCATGAG - CAGGACCGCTGGAGAGATTCAGTTCCTG 962
906 GCGCAGAACCTTACCAACCTTGCATGAGAGGAGGACCTTCCAGAGATGTTTCTCTG 965
963 TAAGAGA - CCGTGCACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1021
966 TAAGAGACCCCTGCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1025
1022 GTTAAGTCCGGCAACGAGGCGCAACCCACGCTCCCTAGTTGCGCAATTCAGTTGGAACT 1081
1026 GTTAAGTCCGGCAACGAGGCGCAACCCACGCTCCCTAGTTGCGCAATTCAGTTGGCACT 1084
1082 CTATGGAATCTGCCGATGATAGTTCGGAGAGGTTGATGATGATGATGATGATGATGAT 1141
1085 TTAGGAGAACTGCGGCTGATAGCCGAGGAGGTTGATGATGATGATGATGATGATGAT 1144
1142 CCTTAGGGTTGGCTTACACAGCTGCTAGATGATGATGATGATGATGATGATGATGAT 1201
1145 CCTTAGGGTTGGCTTACACAGCTGCTAGATGATGATGATGATGATGATGATGATGAT 1204
1202 GCCATCTCAGTTGGCTTACACAGCTGCTAGATGATGATGATGATGATGATGATGATGAT 1261
1205 GCCATCTCAGTTGGCTTACACAGCTGCTAGATGATGATGATGATGATGATGATGATGAT 1264

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1262 TCGCGGAACAGCATGCCGGGTGAATACGTTCCCGGGCTTGTACACACCGCCGCTCACA 1321
1265 TCGCGTAACAGCATGCCGGGTGAATACGTTCCCGGGCTTGTACACACCGCCGCTCACA 1324
1322 CCATGGGAGTGTGTTTACCCGACGACGNTGGCTTAACCTTC--GGGGGCGACGGCCCA 1379
1325 CCATGGGAATTTGGTCTACCCGACGACGCTGGCTTAACCCGAAGGAGGACGCGGCCA 1384
1380 CGGTAGGATCAGGACTGGGGTG 1402
1385 CGGTAGGCTCAGTACTGGGGTG 1407

RESULT 5
US-09-565-063-2
; Sequence 2, Application US/09565063
; Patent No. 6489156
; GENERAL INFORMATION:
; APPLICANT: DISPIRITO, ALAN A.
; APPLICANT: DO, YOUNG S.
; APPLICANT: PHILLIPS, GREGORY J.
; APPLICANT: ZAHN, JAMES A.
; TITLE OF INVENTION: A RHODOBACTER STRAIN FOR ODOR REMEDIATION OF ANAEROBIC
; TITLE OF INVENTION: LIVESOCK WASTE LAGOONS AND BIOMASS PRODUCTION
; FILE REFERENCE: I9000.0044/P044
; CURRENT APPLICATION NUMBER: US/09/565,063
; PRIOR APPLICATION NUMBER: 2000-05-05
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Rhodobacter sp.
; FEATURE:
; OTHER INFORMATION: 16S rDNA of RPS9
US-09-565-063-2

Query Match 82.5%; Score 1198.6; DB 4; Length 1419;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 1308; Conservative 0; Mismatches 105; Indels 7; Gaps 4;

19 AACGAACGCTGGCGGCGGAGGCTTAACACATCAAGTCCGAGCAGACCTTCGGGTCTAGCGG 78
1 AATGAACGCTGGCGGCGGAGGCTTAACACATCAAGTCCGAGCAGGAGTCTTCGGAGTTAGCGG 60
79 CGGACGGGTGAGTAACGCGTGGGAAGTGCCTTCTACGGAATAGCCCGGGAACATG 138
61 CGGACGGGTGAGTAACGCGTGGGAAGTGCCTTCTACGGAATAGCCCGGGAACATG 120
139 GGAGTAATACCGTATACGCCCTTTGGGGGAAAGATTTATCGGAGAAAGATTCGCCCGCGT 198
121 GGAGTAATACCGTATACGCCCTTTGGGGGAAAGATTTATCGCCTTTGGATTGGCCCGCT 180
199 TGAGTAAGTGTGTTGGGGTAATGGCCCAACAGCCGACGATCCATAGCTGTTTGG 258
181 TGAGTAAGTGTGTTGGGGTAATGGCCCAACAGCCGACGATCCATAGCTGTTTGG 240
259 AGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCTACGGGAGGACGAGT 318
241 AGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCTACGGGAGGACGAGT 300
319 GGGAACTTTAGACAATGGGGCAACCTGATCTAGCCATCGCCGCTGAGTGAAGGCC 378
301 GGGAACTTTAGACAATGGGGCAACCTGATCTAGCCATCGCCGCTGATGATGAAGGCC 360
379 TTAGGTTGTAAGTCTTTTACGCTGGGAAGATAATGACGCTACCGGTAAGAAAGCCCC 438
361 TTAGGTTGTAAGTCTTTTACGCTGGGAAGATAATGACGCTACCGGTAAGAAAGCCCC 420
439 GGTAACTCGTCCGACGACCGCGGTAAATACGAGGAGGCTACGCTGTTTGGAAATAC 498

Db 722 GCTTTGAGCATTCGCCCTGGGAGTACGTCGCAAGATTAAACTCAAAGGAATTGACGG 663
QY 860 GGGCCCGCACAGCGGTGAGCATGTTTAAATCGAAGCAACGGCAGAACCTTACCA 919
Db 662 GGGCCCGCACAGCGGTGAGCATGTTTAAATCGAAGCAACGGCAGAACCTTACCA 603
QY 920 ACCCTTGACATGCGCAGGACCGCTGGAGAGATTCAGCTTCTCGTAAGACACCTGCACACA 979
Db 602 TCCCTTGACATGCGCTGTATCCACAGAGATTGGGTCCACTTCGGTGGCGGCACACA 543
QY 980 GGTGCTGATGCTGCTGACGCTGCTGCGAGATGTTCCGTTAAAGTCCGGCAGACAG 1039
Db 542 GGTGCTGATGCTGCTGACGCTGCTGCGAGATGTTGGTTAAAGTCCGGCAGACAG 483
QY 1040 CGCAACCCACGCTCCCTAGTTCGCCCAATTCAGTTGGGAACTCTATGGAACCTGCCGATG 1099
Db 482 CGCAACCCACGCTCCCTAGTTCGCCATC-ATTAGTTGGGCACTCTAGGGAGACTGCCGGTG 424
QY 1100 ATAACTCG-GAGGAAGGTGTGATGACGCTCAAGTCTCTATGGGCTTACGGGTTGGGCTA 1158
Db 423 ATAACTCGGAGGAGGTGTGATGACGCTCAAGTCTCTATGGGCTTACGGGATGGGCTA 364
QY 1159 CACAGCTGCTCAATGTTGGTGTACAGTGG------GTTAATCCCC 1197
Db 363 CACAGCTGCTCAATGTTGGTGTACAGTGGGAGCGGAGGAGGATCTGGGCAATCCCC 304
QY 1198 AAAGCCATCTCAGTTCGGATGCTCTGCAACTCGAGGGGATGAAGTTGGAATCGGTA 1257
Db 303 AAAGCCCTCTCAGTTCGGATGCTCTGCAACTCGAGTGTGATGCAAGGCGGAAATCGGTA 244
QY 1258 GTAATCGGGGACAGCAGTCGCGGTGAATAGTTCCCGGGCTGTACACACCGCCGT 1317
Db 243 GTAATCGGTGATCAGATGCTCAGCGTGAATAGTTCCCGGGCTGTACACACCGCCGT 184
QY 1318 CACACCATGGAGTTGGTTTACCGGACGAGTGTGCTAAGTTCGGGGGCGCAGCGCGC 1377
Db 183 CACACCATGGAGTTGGTTTACCGGACGAGTGTGCTAAGTTCGGGGGCGCAGCGCGC 124
QY 1378 CACGCTAGATCAGGACTGGGTTGAAGTCTGTAACAGGTAGCCCTAGGGGAACTGGG 1437
Db 123 CACGCTAGGTTGACGACTGGGTTGAAGTCTGTAACAGGTAGCCGTAGGGGAACTGGG 64
QY 1438 CTGGA 1442
Db 63 CTGGA 59

RESULT 7

US-08-632-470-52
; Sequence 52, Application US/08632470
; Patent No 5976791
; GENERAL INFORMATION:
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: RAOUIT, DIDIER
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RNA AND
; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,470

; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1415 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-632-470-52

Query Match 71.4%; Score 1036.4; DB 2; Length 1415;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 157; Indels 30; Gaps 7;

QY 14 CTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCG-AGACCTTCGGGTC 72
Db 1 CTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGCACTCTTTTAGAGT 60
QY 73 TAGCGGCGGACGCGGTGAGTAACGCTGGGAAAGTCCCTTCTCAGGAAATAGCCCCGG 132
Db 61 GAGCGGCAAAACGCGGTGAGTAACGCTGGGAAATCTACCATCTCTACGAAATACACAG 120
QY 133 AAACGTGGGAGTAATACCGTATACG-CCCTTTGGGGGAAAGATTATTCGAGAGGATCG 191
Db 121 AAATTTGTGCTAATACCGTATACGTCCTCTGGGAGAAAGATTATTCGAGAGGATGAG 180
QY 192 CCCGCTGGTGGATTAGTAGTGTGGGTAAATGGCCCAACCAACGACCATCATAGCTG 251
Db 181 CCCGCTGGTGGATTAGTAGTGTGGGTAAAGGCTCACCAAGGCGACCATCATAGCTG 240
QY 252 GTTTCAGAGGATGATCAGCCACACTGCGGACTAGACACCGCCGACACTCTACGGAGGC 311
Db 241 GTCTGAGAGGATGATCAGCCACACTGCGGACTAGACACCGCCGACACTCTACGGAGGC 300
QY 312 AGCAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCCGCGTGAAGTAT 371
Db 301 AGCAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCCGCGTGAAGTAT 360
QY 372 GAAGCCCTTAGGGTTGTTAAAGCTCTTTCAGCTGGGGAAGATATAGCGTACCAGCAAGAG 431
Db 361 GAAGCCCTTAGGGTTGTTAAAGCTCTTTCAGCGGTGAAGATATAGCGTACCAGCAAGAG 420
QY 432 AAGCCCCGCTAACCTCCGTCGCGCAGCAGCGCGGTAAATACGAGGGGGCTAGCGTTGTCG 491
Db 421 AAGCCCCGCTAACCTCCGTCGCGCAGCAGCGCGGTAAATACGAGGGGGCTAGCGTTGTCG 480
QY 492 GAATTACTGGGCTAAAGCGCACGCTAGCGGACTGGAAGTCAGAGGTGAATATCCAGG 551
Db 481 GATTACTGGGCTAAAGCGCATGATGAGCGGATATTAAGTCAGAGGTGAATATCCAGG 540
QY 552 CTCACCTTGGAACTGCCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAGGTGAGTGAAT 611
Db 541 CTCACCTTGGAACTGCCCTTTGATCTGATCTGAGTCTGAGTGTGGAAGAGGTGAGTGAAT 600
QY 612 TCCGAGTGTAGAGGTGAATTCGCTAGATATTCGAGAGGAACACCATGCGGAAAGGGGCTC 671
Db 601 TCCGAGTGTAGAGGTGAATTCGCTAGATATTCGAGAGGAACACCATGCGGAAAGGGGCTC 660
QY 672 ACTGCTGATCTACGCTGAGGTGCGAAACGCTGGGAGGAGCAACACAGATTAGATACC 731
Db 661 ACTGCTGATCTACGCTGAGGTGCGAAACGCTGGGAGGAGCAACACAGATTAGATACC 720
QY 732 TGGTAGTCCACGCCCTAAACAGATGAATGCACAGCTCGCAGAGCATGCTTTCGGTGTCA 791
Db 721 TGGTAGTCCACGCCCTAAACAGATGAATGTTAGCCCTCGGGTGTGTACTACTCTCGTGGCG 780

Db 772 CGAAGCGGCTCACTGACCTGGATTATGACGCTGAGGTGCGAAGCGTGGGAGCAACA 831
QY 719 GGATTAGATACCTGTTAGTCCAGCCGCTAAACGATGAATGCCAGACGTCGCGAAGCATG 778
Db 832 GGATTAGATACCTGTTAGTCCAGCCGCTAAACGATGAATGAATGCTGCGGAGCATG 891
QY 779 CT-TGTGCTGTACACCTACGATTAAGCATTCCTGCTGGGAGTACGCTGCGCAAGAT 837
Db 892 GTCTTTGGGTGGCGAGCTACGCAATTAAGTTATCCGCTGGGAGTACGCGCGCAAGGT 951
QY 898 TAAACTCAAAAGGAATTCACGGGGGCGCCGCAACGCGTGGAGCATGTGGTTAATTGGA 897
Db 952 TAAACTCAATGAATTCACGGGGGCGCTGCACACCGCTGGAGCATGTGGTTAATTGGA 1011
QY 898 AGCAACGGCGAGAACCTTACCAACCTTTGACATGATGCGAGACCGCT--GGAGAGATTCAGC 955
Db 1012 AGCAACGGCGAGAACCTTACCAACCTTTGACATGATGCGAGACATTTCTGGAGACAGATCT 1071
QY 956 TTTCTCGTAAGAGACCTGCACACAGGTGCTGCATGCTGTGCTGACGCTGCTGCTGAGA 1015
Db 1072 CTTCCTTCGGGAGCTGGAACGCGAGGTGCTGATGCTGCTGCTGCTGCTGCTGAGA 1131
QY 1016 TGTTCGGTTAAGTCCGCAAGGAGCGCAACCCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
Db 1132 TGTTCGGTTAAGTCCGCAAGGAGCGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1190
QY 1076 GGAATCTATGGAATCCGATGATGAATGATGCGGAGGAGGTGATGATGATGATGATGATG 1135
Db 1191 GGGACTCTAAAGGAACCGCGCTGATGAAGCGGAGGAGGTGCGGATGACGCTCAAGTCT 1250
QY 1136 CATGGCCCTTACGGTTGGGCTACACAGCTGCTCAATGTTGGTGCACAGTGG----- 1187
Db 1251 CATGGCCCTTACGGCTGGGCTACACAGCTGCTCAATGTTGGGCTGACAGTGGCGGAGCA 1310
QY 1188 -----GTTAATCCCAAAAGCCATCTCAGTTCGGATGCTCTGCAACTCG 1234
Db 1311 CTCGGAGAGTGGCTAATCTCAAAAGCGCTCAGTTCGGATGTTCTGCAACTCG 1370
QY 1235 AGGCATGAATGGAATCGTATGTAATCGGGAACAGCATGCGCGGTGTAATGTTCC 1294
Db 1371 AGAGCATGAAGCGGAATCGTATGTAATCGGGAATCAGCATGCGCGGTGTAATGTTCC 1430
QY 1295 CGGCTTGTACACACCGCGCTACACCATGTTGGGAGTGTCTACCGGAGCAGCAGTGG 1354
Db 1431 CAGGCTTGTACACACCGCGCTACACCATGTTGGGAGTGTCTACCGGAGCAGCAGTGG 1490
QY 1355 CTA--CCTTCGGGGGCGAGCGGCGCAGCTAGGATCAGCGACTGGGTGAGTCTAATC 1412
Db 1491 CTAATCTGAAGAGGAGCGGAGCAGCGGCTTACCGACTGGGTGAGTCTAATC 1550
QY 1413 AAGGTA 1418
Db 1551 AAGGTA 1556

RESULT 9

US-08-632-470-44

; Sequence 44, Application US/08632470

; Patent No. 5976791

; GENERAL INFORMATION:

; APPLICANT: MABILIAT, CLAUDE

; APPLICANT: RAOUIT, DIDIER

; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF

; HYBRIDIZING SPECIFICALLY TO RICKETTIA RDNA OR RNA AND

; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1508 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-632-470-44

Query Match 67.5%; Score 980.2; DB 2; Length 1508;

Best Local Similarity 81.8%; Pred. No. 0;

Matches 1220; Conservative 0; Mismatches 229; Indels 43; Gaps 6;

QY 1 AGTTTGATCTCGCTCAGAACGAGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
Db 19 AGTTTGATCTCGCTCAGAACGAGCTATCGGTATGCTTAACATGCAAGTCGAGCGG 78
QY 61 GACCTTCGGGTCTAGC-----GGCGACGCGGTGAGTAACGCTGGGGAACCT 106
Db 79 ATTAAGTACGAGCTCGCTTTAGTTAATTAGTGGCAGCGGTGAGTAACGCTGGGAATCT 138
QY 107 GCCCTTCTCAGGAATAGCCCCGGGAAACTGGGAGTAACTAGCTATACGCTATACGCTTTGGGG 166
Db 139 ACCCATCATAGTACGGAATACCTTTTAAATAAAGCTAATACCGTATATCTCTACGGAG 198
QY 167 GAAAGATTATCGGAGAGGATCGGCCCGCTGGATTAGTATAGTGGTGGGTAAATGCG 226
Db 199 GAAAGATTATCGCTGATGAGTGGCCCGCTCAGATAGTATAGTGGTGGGTAAATGCG 258
QY 227 CCACCAAGCCGACGATCCTAGCTGTTTGAAGAGTATGATCCACACTGGGACTGAGA 286
Db 259 TCACCAAGCCGACGATCTGTAGCTGTCTGAGAGGATGATCAGCCACACTGGGACTGAGA 318
QY 287 CACGCCCCAGACTCCTACGGGAGGAGCAGTGGGGAATCTTAGACAATGGGGGCAACCT 346
Db 319 CACGCCCCAGACTCCTACGGGAGGAGCAGTGGGGAATCTTAGACAATGGGGGCAACCT 378
QY 347 GATCTAGCCATCGCCGCTGAGTGAAGGCTTAGGCTTGAAGCTCTTTTCAGCTGGG 406
Db 379 GATCCAGCAATACCGAGTGAAGGCTTAGGCTTGAAGCTCTTTTCAGCAAGG 438
QY 407 AAGATAATGACGCTACCGAGCAGAAAGCCCGGCTTAACCTCGCTCCAGCAGCCCGGTA 466
Db 439 AAGATAATGACGCTTACTTGCAGAAAAAGCCCGGCTTAACCTCGCTCCAGCAGCCCGGTA 498
QY 467 ATACGGAGGGCTAGCTGTTTTCGGAATTTACTGGGCTTAAAGCGGAGCAGCTAGCGGACTG 526
Db 499 AGACGAGGGGCTAGCTGTTTTCGGAATTTACTGGGCTTAAAGAGTGCCTAGCGGCTTTA 558
QY 527 GAACTCAGAGTGAATCCCAAGGCTCAACCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 586
Db 559 GTAAGTTGGAAGTGAAGCGCGGCTTAACCTCGGAATTTCTCAAAACACTACTAATCT 618
QY 587 GGAGTTCGAGAGAGGTGAGTGAATTTCCAGGTGTAGAGGTGAATTTCCGTAGATATTCCGA 646
Db 619 AGAGTGTAGTAGGGATGATGGAATTTCCAGGTGTAGAGGTGAATTTCCGTAGATATTAGGA 678

647 GGAACACAGTGGCGAAGGCGGCTCACTGGCTCGATACATGACGCTGAGTGGCGAAGCGT 706
679 GGAACACCGGTGGCGAAGGCGGCTCATCTGGCTGACACTGACGCTGATGACGAAAGCGT 738
707 GGGAGCAACAGAGTAGATACCTGGTGTAGTACAGCCGCTAAACGATGAATGACGAGC 766
739 GGGAGCAACAGAGTAGATACCTGGTGTAGTACAGCCGCTAAACGATGAATGACGAGC 798
767 TGGCAAGCAGTGTGCTGGTGTACACACCTAAGGATTAAGCATTCGCGCTGGGAGTAC 826
799 TCGG-AGGATCTCTTTCGGTTCGCGAGCTAACGATTAAGCATTCGCGCTGGGAGTAC 857
827 GGTGCGAAGATTAAACTCAAGGAATTTAGCGGGGCGCCACACAGCGGTGGAGCATGTG 886
858 GGTGCGAAGATTAAACTCAAGGAATTTAGCGGGGCTGCGACAAAGCGGTGGAGCATGCG 917
887 GTTTAATTCAGGCAAGCGCGAGACCTTACCAACCTTGACATGCGCAGACCG-CT 942
918 GTTTAATTCAGGCAAGCGCGAGACCTTACCAACCTTGACATGCGGTGGTACGATGCG 977
943 GGAGAGATTTCAGCTTTCTCGTAAGAGACCTGACACAGGTGCTGATGGCTGCTGTCAGC 1002
978 AGAGATGCTTTCCTTCAGTTCGGCTGGCGCCACACAGAGGTGTCATGGCTGCTGTCAGC 1037
1003 TCGTGTGCTGAGATGTTTCGGTTAAGTCCGGCAACAGCGGCAACCCACGCTCCCTAGTTGCC 1062
1038 TCGTGTGCTGAGATGTTTCGGTTAAGTCCGGCAACAGCGGCAACCCCTATTCTATTGCC 1097
1063 AGCAATTCA-GTTGGGAATCTATGAAACTGCGGATGATAAGTGGAGGAAGGTGGA 1121
1098 AGTGGGTAATGCCGGAACTATAGAAACTGCGGTTGATAAGCGGAGGAAGGTGGGA 1157
1122 TGAGTCAAGTCTCATGCGGCTTACGGTTTGGCTACACAGCTGCTACATGCTGCTGA 1181
1158 CGAGTCAAGTCTCATGCGGCTTACGGTTTGGCTACACAGCTGCTACATGCTGCTGA 1217
1182 CAGTGG-----GTTAATCCCAAGGCAATCCCTAAAGACATCTCAGTTCGGATTG 1220
1218 CAGAGGAGCAATACGTTGAGTGGAGCAATCCCTAAAGACATCTCAGTTCGGATTG 1277
1221 TCCTCTGCACTGAGGGCATGAAGTTGGAATGCTAGTAAATCCCGGAACAGCATGCGGC 1280
1278 TTCTCTGCACTGAGAGCATGAAGTTGGAATGCTAGTAAATCCCGGAACAGCATGCGGC 1337
1281 GGTGAATACGTTCCCGGCTTGTACACACCGCGCTGACACAGCTGCTGCTGCTAC 1340
1338 GGTGAATACGTTCCCGGCTTGTACACACCGCGCTGACACAGCTGCTGCTGCTTAC 1397
1341 CCGACGAGTTCGCTAACCTTCGGGGGCGAGCGGCGGCTAGGATCAGCAGTGGG 1400
1398 CTGAAGGTGGTGAAGTAAAC--GCAAGAGCGAGCAACACCGGTAATAGCAGTGGG 1455
1401 TGAAGTCTGACAGGATGAGCGTAGGAGGAGCTGCGGCTGATCAGTCCCTT 1452
1456 TGAAGTCTGACAGGATGAGCGTAGGAGGAGCTGCGGCTGATCAGTCCCTT 1507

RESULT 10
US-09-347-001-2
; Sequence 2, Application US/09347001A
; Patent No. 6335177
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: TAKEUCHI, Sonoko
; APPLICANT: JOIHA, Yasuko
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: FUDOU, Ryoosuke
; APPLICANT: YOKOZAKI, Kenzo
; TITLE OF INVENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR
; TITLE OF INVENTION: D-XYLULOSE
; FILE REFERENCE: 0010-1015-0
; CURRENT APPLICATION NUMBER: US/09/347.001A
; CURRENT FILING DATE: 1999-07-02

EARLIER APPLICATION NUMBER: JP 10-193472
EARLIER FILING DATE: 1998-07-08
EARLIER APPLICATION NUMBER: JP 10-310398
EARLIER FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: JP 11-12244
EARLIER FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1436
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: strain S877
US-09-347-001-2

Query Match 67.1%; Score 973.6; DB 4; Length 1436;
Best Local Similarity 82.4%; Pred. No. 0;
Matches 1186; Conservative 0; Mismatches 225; Indels 28; Gaps 5;

QY 5 TGATCTGGCTCAGAACGACGCTGGGGCAGGCTTAACACATGCAAGTCGAGCGAGACC 64
DB 1 TGATCTGGCTCAGAACGACGCTGGGGCAGGCTTAACACATGCAAGTCGAGCGAGACC 60
QY 65 TTGCGGCTAGCGCGGACGCGGTGAGTAACGCTGGGAACGCTTCTCTACGGAATA 124
DB 61 TTGCGGCTAGCGCGGACGCGGTGAGTAACGCTGGGAACGCTTCTCTACGGAATA 120
QY 125 GCGCGGGAACCTGGGAGTAAATACGCTATACGCGCTTTGGGGGAAG--ATTATCGAG 182
DB 121 ACACCGGAACCTGGTGTCTAATACGCTATACGCTAGGCTTTAAAGGCTTTTGTGCT 180
QY 183 AAGGATCGCGCGCTGGATTAGTGTAGTGGTGAATGCTGGGCTAAATGGCCACCAAGCCAGCAT 242
DB 181 TTGAGGGCGCTCGCTTTGATTAGTGTGGTGAAGGCTTGACCAAGGCGGTAT 240
QY 243 CCATAGCTGTTTGGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCT 302
DB 241 CAATAGCTGTTTGGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCT 300
QY 303 ACGGAGGACGAGTGGGGAATCTTAGACAATGGGGCAACCTGATAGCCATGCGCGC 362
DB 301 ACGGAGGACGAGTGGGGAATCTTAGACAATGGGGCAACCTGATAGCCATGCGCGC 360
QY 363 GTGAGTGTAGAGCGCTTAGGCTTGAAGCTTTTACGCTGGGAAGATAATGACGCTAC 422
DB 361 GTGAGTGTAGAGCGCTTAGGCTTGAAGCTTTTACGCTGGGAAGATAATGACGCTAC 420
QY 423 CAGCAGAAGAACGCGCGCTAACTCCGTCGACGAGCGCGGTAAATCGGAGGGGCTAG 482
DB 421 CTAGAGAAGAACGCGCGCTAACTCCGTCGACGAGCGCGGTAAATCGGAGGGGCTAG 480
QY 483 CGTTGTTGGAATTAAGGCGGTAAAGCGGCTAGGCGGCTGGAAGTACAGAGGTAA 542
DB 481 CGTTGTTGGAATTAAGGCGGTAAAGGCGGCTAGGCGGCTGGAAGTACAGAGGTAA 540
QY 543 ATCCGAGGCTCAACCTTGGAACTGCTTTTGAACATATCAGTCTGGAGTTCGAGAGGT 602
DB 541 ATCCGAGGCTCAACCTTGGAACTGCTTTTGAACATATCAGTCTGGAGTTCGAGAGGT 600
QY 603 GAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAGAACACGAGTGGGA 662
DB 601 TTGCGGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAGAACACGAGTGGGA 660
QY 663 AGCGGCTCACTGCTGATACTGACGCTGAGTGGGAGGCGGCTGGGAGCAACAGGAT 722
DB 661 AGCGGCAATCTGCTGGAATCAGCTGAGGCGGCAAGCGTGGGAGGCAACAGGAT 720
QY 723 TAGATACCTGCTAGTCCACGCGTAAACGATGAATGCGACAGCTGCGCAAGCAT--GCTT 781
DB 721 TAGATACCTGCTAGTCCACGCTGTAACGATGCTGCTGATGCTGTTGGAAACATGATT 780
QY 782 GTCGCTGTACACACCTAACGGATTAAAGCATTCGCGCTGGGGAGTAGGCTGCGCAAGATTAA 841

Db 781 TTCAAGTGTGGAAGTAACTGTAAAGCAACCGCTGGGAGTACGACCGAAGTGA 840
QY 842 ACTCAAGGAATTACGGGGGCGCCACAAAGCGGTGGAGCATGGTTTAATCAAGCA 901
Db 841 ACTCAAGGAATTACGGGGGCGCCACAAAGCGGTGGAGCATGGTTTAATCAAGCA 900
QY 902 ACGGCGAAGCTTACCAACCTTGCACATGCGAGGACCGCTGGAGAGATTCAAGCTTCTC 961
Db 901 ACGGCGAAGCTTACCAAGTCTGTATGGGAGGACGCTGCTCAGAGATGAGTATTC-- 958
QY 962 GTAAGAGACCTGCACACAGGTGCTGCATGGCTGTGTCAGCTGCTGTCGAGAGTTCG 1021
Db 959 -TTCGGACCTCCCGACACAGGTGCTGCATGGCTGTGTCAGCTGCTGTCGAGAGTTCG 1017
QY 1022 GTTAAGTCCGCAACGAGCGCAACCCAGCTCCCTAGTTCGACGCA-ATTCAAGTTCGGGAAC 1080
Db 1018 GTTAAGTCCGCAACGAGCGCAACCCCTGCTTTAGTTGCCATCAGTTTGGGTGGGCAC 1077
QY 1081 TCTATGGAACCTGCGGATGATAAGTTCGGAGGAGGTGTGGATGACGTCAAGTCCCTCATGG 1140
Db 1078 TCTAGAGAGATGCGGTGACACGCGGAGGAGGTGGGATGAGTCAAGTCCCTCATGG 1137
QY 1141 GCCTTACGGGTGGGCTACACACGTGCTACAAATGGTGTGACAGTGG----- 1187
Db 1138 CCTTATGACCTGGGCTACACAGGTGCTACAAATGGGAGGAGTACATGCT 1197
QY 1188 -----GTTAATCCCAAGGACATCTAGTTCGGATGTGCTGTCGAACTCGAGGCG 1239
Db 1198 GACATGATGCGGATCTCAAAAACCGTCTCAGTTCGGATGCACTCTGCACTGCTGCACTGCTG 1257
QY 1240 ATGAAGTGGATGCTAGTAACTCCGGAACAGCATGCGGGTGAATACGTTCCCGGGC 1299
Db 1258 ATGAAGTGGATGCTAGTAACTCCGGAACAGCATGCGGGTGAATACGTTCCCGGGC 1317
QY 1300 CTGTTACACCGCCGCTACACACCTGGAAGTGGTGTCTTACCCGACGAGTGGCTTAAC 1359
Db 1318 CTGTTACACCGCCGCTACACACCTGGAAGTGGTGTCTTACCCGAGTGGAGTGAAC 1377
QY 1360 CTTCGGGGGAGGCGGCGCAGGTAGGATCAGCGACTGGGTGAAGTGTACAAAGGTA 1418
Db 1378 CGAAGGCGCAGCGACCCAGCGTGGGTGCGGCTCAGCGACTGGGTGAAGTGTACAAAGGTA 1436

RESULT 11

US-09-347-001-1
; Sequence 1, Application US/09347001A
; Patent No. 6335177

GENERAL INFORMATION:

; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: TAKEUCHI, Sonoko
; APPLICANT: JOJIMA, Yasuko
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: FUDOU, Ryosuke
; APPLICANT: YOKOZAKI, Kenzo
; TITLE OF INVENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR
; TITLE OF INVENTION: D-XYLULOSE
; FILE REFERENCE: 0010-1015-0
; CURRENT APPLICATION NUMBER: US/09/347,001A
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: JP 10-193472
; EARLIER FILING DATE: 1998-07-08
; EARLIER APPLICATION NUMBER: JP 10-310398
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: JP 11-12244
; EARLIER FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

; LENGTH: 1438
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: strain P528
; FEATURE:
; OTHER INFORMATION: N at position 1365 is A, T, G, or C
US-09-347-001-1

Query Match 66.1%; Score 960.4; DB 4; Length 1438;
Best Local Similarity 82.3%; Pred. No. 6.1e-315;
Matches 1183; Conservative 0; Mismatches 228; Indels 27; Gaps 6;

QY 5 TGATCCTGCTCAGAACCAACGCTGGCGCAGCGCTTTAACATGCAAGTCGAGCGAGACC 64
Db 1 TGATCCTGCTCAGAGCAACGCTGGCGCATGCTTAACATGCAAGTCGAGCGAGACC 60
QY 65 TTCGGGTCTAGCGCGGACGGGTGAGTAACGCGTGGGAACGTCCTCTCTACGGAATA 124
Db 61 TTCGGGTGAGTGGCGGAGCGGTGAGTAACGCGTAGGGATCTATCCACGGGTGGGGATA 120
QY 125 GCCCGGGAACCTGGGAGTAAATACGCTATACGCCCTTTGGGGGAAG--ATTATCGGAG 182
Db 121 ACACGTGGAAACTGGTGTCTAATACCGCATGATACCTGAGGTCAAAGGCGCGAGTCGCCT 180
QY 183 AAGGATCGCCCGCGCTTGGATTAGGTAGTGGTGGGTAAATGCCCAACCAAGCCGACGAT 242
Db 181 GTGGAGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 243 CCATAGCTGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCGACGACTCCT 302
Db 241 CCATAGCTGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCGACGACTCCT 300
QY 303 ACGGAGGCGAGCAGTGGGGAATCTTAGACAATGGGGCAACCTGATCTAGCCATGCCGC 362
Db 301 ACGGAGGCGAGCAGTGGGGAATCTTAGACAATGGGGCAACCTGATCTAGCCATGCCGC 360
QY 363 GTGAGTGTGAAGGCTTTAGGTTGTAAAGCTCTTTACGCTGGGAAGATAATACGGGTAC 422
Db 361 GTGAGTGTGAAGGCTTTAGGTTGTAAAGCTCTTTACGCTGGGAAGATAATACGGGTAC 420
QY 423 CAGCAGAGAAGCCCGCTTAACCTCGCTGCCAGCAGCGCGGTAAATACGGAGGGGCTAG 482
Db 421 CCGTGAAGAAGCCCGCTTAACCTCGCTGCCAGCAGCGCGGTAAATACGGAGGGGCTAG 480
QY 483 CCGTGTGCGAATTAATCTGGGCGTAAAGCGCACGCTAGGCGGACTTGGAAAGTCAGAGGTGA 542
Db 481 CCGTGTGCGAATTAATCTGGGCGTAAAGCGCGTGTAGCGGCTTTACAGTCAGATGTGA 540
QY 543 ATCCAGGCTCAACCTTGGAACTGCTTTGAAACTATCAGCTGTGAGTGTGAGAGAGGT 602
Db 541 ATCCAGGCTTAACTTGGGCTGCTATTTGATACGCTAGCAGTGTGAGAGAGGT 600
QY 603 GAGTGAATTCGAGTGTAGAGTGAATTCGATATTCGAGGAACACCAAGTCGCGCA 662
Db 601 TTGTTGAATTCGAGTGTAGAGTGAATTCGATATTCGAGGAACACCAAGTCGCGCA 660
QY 663 AGCGGCTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
Db 661 AGCGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 723 TAGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
Db 721 TAGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 783 -TCGGTGTACACCTTAACGATTACGCTTCCGCTGGGAGTACGCTGCGAGATTAA 841
Db 781 CTCAGTGTGGAAGCTAAACGCTGAGCAGCCCTTGGGAAGTACGCGCGAGGTTGAA 840
QY 842 ACTCAAGGAATTGACGGGGCGCCGACAAAGCGGTGGAGCATGTGTTTAAATCGAAGCA 901
Db 841 ACTCAAGGAATTGACGGGGCGCCGACAAAGCGGTGGAGCATGTGTTTAAATCGAAGCA 900
QY 902 ACGCGCAGAACCTTACCAACCTTACAT-GGCAGGACCGCTGGAGAGATTACGCTTTCT 960
Db 901 ACGCGCAGAACCTTACCAACCTTACATGGGAGGCTGTACTCAGAGATGGGTATTTCC 960

960	CTTCTTAACAGAAAGGCGCATGTTCCGGCTCGCACAGGTGCTCGATCGCTGCTGC	1019
1000	AGTCGTGTCGTGAGATGTTTCGGTTAAGTCCGGCAACGAGCGCAACCCACGCTCCCTAGTT	1059
1020	AGTCGTGTCGTGAGATGTTGGTTAAGTCCGGCAACGAGCGCAACCCCTCATCTTACTT	1079
1060	GCCAGCAATTCATGTTGGGAACCTATGGAACCTGCCGATGATTAAGTCGGAGGAAGTGT	1118
1080	ACGAGCGGTAAATGCCGGGCACATTAAAGGAACCTGCCAGTGAATAACTGGAGGAAGTGG	1139
1119	GGATGACGTCGAAGTCCTCATGGGCGCTTACGGGTGGGCTACACACGTCGTACAATGGTGG	1178
1140	GGATGATGTCGAAGTCAGCAGCGGCCCTTATGGGTGGGCTACACACGTCGTACAATGGCGA	1199
1179	TGACAGTGGGT-----TAATCCCCAAAAGCCATCTCAGTTCGGA	1217
1200	CTACAAATAGTTGCAACGTCGAAGCTGAGCTAATCCGTAAATCGTCTCAGTTCGGA	1259
1218	TTGTCCTCTGCAACTCGAGGGCATGAAGTTGGAATCGTATGTAATCGCGGAACACGATCGC	1277
1260	TTGTCCTCTGTAACCTCGAGGGCATGAAGTCGGAATCGTACTAATCGTGGATCAGCATGC	1319
1278	CGGGGTGAATACGTTCCCGGGCCCTTGATACACACCGCCGCTCACACACATGGAGTGGTTC	1337
1320	CACGGTGAATACGTTCTCGGGTCTTGATACACACTGCCCGCTCACGCCATGGGAATTGGCT	1379
1338	TACCCGACAGGNTGGCTAACCTTCGGGGGAGGGCGGCACCGTAGGATCAGGCACTG	1397
1380	AACTCGAAGCTGGTGGCCCAACCGTAGGAGGCAGCCATTAAAGTTGGTTCGCTCACTG	1439
1398	GGGTGAAGTCGTAACAAAGGTAGCCGTAGGGGAACCTCGGGCTGGATCACTCCCTT	1452
1440	GGGTGAAGTCGTAACAAAGGTAGTGTAGGTGAACCTCGGGCTGGATCACTCCCTT	1494

RESULT 13

US-08-632-470-33
Sequence 33, Application US/08632470
Patent No. 5976791
GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 10:53:33 ; Search time 356 Seconds
(without alignments)
8414.261 Million cell updates/sec

Title: US-10-049-228-1
Perfect score: 1452
Sequence: 1 agtttgatctggctcagaa.....tgoggtggtacacctctt 1452

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq*
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- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1380	95.0	1426	14	US-10-049-228-2
3	1093.6	75.3	1466	9	US-09-726-774-12
4	1086.4	74.8	1502	10	US-09-894-467-2
5	1044.6	71.9	1490	9	US-09-900-876-2
6	973.6	67.1	1436	9	US-09-902-693-2
7	960.4	66.1	1438	9	US-09-902-693-1
8	904.8	62.3	1208	10	US-09-894-467-1
9	881.4	60.7	105184	11	US-09-847-513A-1
10	869.8	59.9	1532	13	US-10-007-725-6
11	863.4	59.5	1494	13	US-10-007-725-5
12	861.8	59.4	1501	9	US-09-791-592-1
13	861.8	59.4	1501	9	US-09-745-476-1
14	861.8	59.4	1501	9	US-09-821-016-5
15	861.8	59.4	1501	9	US-09-748-205-1
16	861.8	59.4	1501	9	US-09-793-920A-1

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18	861.8	59.4	1501	11	US-09-791-610-1	Sequence 1, Appli
19	861.8	59.4	1501	14	US-10-218-519-5	Sequence 5, Appli
20	861.8	59.4	1501	14	US-10-266-787-5	Sequence 5, Appli
21	861.8	59.4	1501	14	US-10-252-518-5	Sequence 5, Appli
22	861.8	59.4	1501	14	US-10-105-305-1	Sequence 1, Appli
23	861.8	59.4	1501	14	US-10-133-404A-1	Sequence 1, Appli
24	857.6	59.1	1540	10	US-09-967-376-1	Sequence 1, Appli
25	857.6	59.1	1540	14	US-10-260-647-1	Sequence 4, Appli
26	848.8	58.5	1481	9	US-09-737-297-4	Sequence 3, Appli
27	841	57.9	1467	9	US-09-726-774-3	Sequence 7, Appli
28	840.4	57.9	1541	9	US-09-027-439-7	Sequence 158, App
29	839.4	57.8	1542	11	US-09-940-925A-158	Sequence 158, App
30	839.4	57.8	1542	11	US-09-941-193A-158	Sequence 158, App
31	839.4	57.8	1542	14	US-10-061-071-33	Sequence 33, Appli
32	830.8	57.2	1541	9	US-09-726-774-2	Sequence 2, Appli
33	830	57.2	1549	9	US-09-913-020-89	Sequence 89, Appli
34	830	57.2	1549	9	US-09-913-020-242	Sequence 242, Appli
35	830	57.2	1549	9	US-09-912-020-402	Sequence 402, App
36	819.4	56.4	1544	9	US-09-728-774-5	Sequence 5, Appli
37	815.4	56.2	1553	10	US-09-974-300-4446	Sequence 4446, Ap
38	814.2	56.1	1500	9	US-09-726-774-4	Sequence 4, Appli
39	813.8	56.0	1552	10	US-09-974-300-8479	Sequence 8479, Ap
40	812.8	56.0	1830121	14	US-10-329-960-1	Sequence 1, Appli
41	812.8	56.0	1830121	14	US-10-329-960-1	Sequence 1, Appli
42	809.8	55.8	1506	9	US-09-027-439-3	Sequence 3, Appli
43	809.2	55.7	1424	14	US-10-007-527A-12	Sequence 12, Appli
44	809.2	55.7	1424	14	US-10-007-452-12	Sequence 12, Appli
45	806	55.5	7455	14	US-10-219-227-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1

US-10-049-228-1
; Sequence 1, Application US/10049228
; Publication No. US2003004486A1
; GENERAL INFORMATION:
; APPLICANT: TSUBOKURA, Akira
; APPLICANT: MIYATA, Haruyoshi
; TITLE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS
; FILE REFERENCE: 38331-0003
; CURRENT APPLICATION NUMBER: US/10/049,228
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/04874
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: JP 2000-175124
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA o

QY	1	AGTTTGATCTCGGCTCAGAACGAGCTGGCGGAGGCTTACACATGCAAGTCGAGCGA	60
DB	1	AGTTTGATCTCGGCTCAGAACGAGCTGGCGGAGGCTTACACATGCAAGTCGAGCGA	60
QY	61	GACCTTCGGGCTACGCGGCGGAGGCTGAGTACCGCTGGGACCTGCCCTTCTCTACGG	120

Db 61 GACCTTGGGCTTACGGCGGAGCGGGTGAAGACGCGTGGGAACGTGCCCTTCTCTACGG 120
Qy 121 AATAGCCCGGGAACATGGAGTAAATACCGTATACGCCCTTTGGGGAAGATTTATCGG 180
Db 121 AATAGCCCGGGAACATGGAGTAAATACCGTATACGCCCTTTGGGGAAGATTTATCGG 180
Qy 181 AGAAGGATCGCCCGCGTGGATTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGT 240
Db 181 AGAAGGATCGCCCGCGTGGATTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGT 240
Qy 241 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCAGACTC 300
Db 241 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCAGACTC 300
Qy 301 CTACGGAGGACAGTGGGAATCTTAGACAATGGGGCAACCTGATCTAGCCATGCC 360
Db 301 CTACGGAGGACAGTGGGAATCTTAGACAATGGGGCAACCTGATCTAGCCATGCC 360
Qy 361 GCGTGAAGTGAAGGCTTAGGGTTGTAAGCTCTTTACGCTGGGAAGATAATGACGGT 420
Db 361 GCGTGAAGTGAAGGCTTAGGGTTGTAAGCTCTTTACGCTGGGAAGATAATGACGGT 420
Qy 421 ACCAGCAGAAAGCCCGGCTAACTCGTCCAGCAGCCCGGTATACGGAGGGGCT 480
Db 421 ACCAGCAGAAAGCCCGGCTAACTCGTCCAGCAGCCCGGTATACGGAGGGGCT 480
Qy 481 AGCGTTGTCGAATTAAGTGGCGTAAAGCCAGCTAGGCGGACTGGAAGTCAAGAGTG 540
Db 481 AGCGTTGTCGAATTAAGTGGCGTAAAGCCAGCTAGGCGGACTGGAAGTCAAGAGTG 540
Qy 541 AAATCCAGGCTCAACCTTGAAGTCTTTGAACTATCAGTCTGGAGTTCAGAGAG 600
Db 541 AAATCCAGGCTCAACCTTGAAGTCTTTGAACTATCAGTCTGGAGTTCAGAGAG 600
Qy 601 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGGAGAAACACAGTGGC 660
Db 601 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGGAGAAACACAGTGGC 660
Qy 661 GAAGCGCTCAGTGGCTGATGAGTGGCTGAGTGGCTGGAAGCGTGGGAGCAACAGG 720
Db 661 GAAGCGCTCAGTGGCTGATGAGTGGCTGAGTGGCTGGAAGCGTGGGAGCAACAGG 720
Qy 721 ATTAGATACCTGGTGTCCAGCGCTAAACGATGAATGCCAGACGCTGGCAAGCATGCT 780
Db 721 ATTAGATACCTGGTGTCCAGCGCTAAACGATGAATGCCAGACGCTGGCAAGCATGCT 780
Qy 781 TGTGGTGTACACCTAACGATTAAGCATTCGCGCTGGGGAGTACGGTCCCAAGATTAA 840
Db 781 TGTGGTGTACACCTAACGATTAAGCATTCGCGCTGGGGAGTACGGTCCCAAGATTAA 840
Qy 841 AACTCAAGGAATTCAGGGGCGCCGACAGCGGTGGAGCATGCTGTTTAAATTCGAGC 900
Db 841 AACTCAAGGAATTCAGGGGCGCCGACAGCGGTGGAGCATGCTGTTTAAATTCGAGC 900
Qy 901 AACCGCGAAGACCTTACCACCTTGACATGGCAGGACCGCTGGAGAGATTTCAGCTTCT 960
Db 901 AACCGCGAAGACCTTACCACCTTGACATGGCAGGACCGCTGGAGAGATTTCAGCTTCT 960
Qy 961 CGTAAGAGACCTGCACACAGTGTGATGGCTGTGTCAGCTCGTGTGAGATGTTTC 1020
Db 961 CGTAAGAGACCTGCACACAGTGTGATGGCTGTGTCAGCTCGTGTGAGATGTTTC 1020
Qy 1021 GGTAAAGTCCGGCAACGAGCGCAACCCAGTTCCTAGTTCGACCAATTCAGTTGGGAC 1080
Db 1021 GGTAAAGTCCGGCAACGAGCGCAACCCAGTTCCTAGTTCGACCAATTCAGTTGGGAC 1080
Qy 1081 TCTATGAAACTGCCGATGATAAGTTCGGAGGAAGTGTGATGACGTCAGTCTCATGG 1140
Db 1081 TCTATGAAACTGCCGATGATAAGTTCGGAGGAAGTGTGATGACGTCAGTCTCATGG 1140
Qy 1141 GCCTTAGGGTTGGGCTACACACGTGTGATCAATGGTGTGACAGTGGGTTTAAATCCCAAA 1200
Db 1141 GCCTTAGGGTTGGGCTACACACGTGTGATCAATGGTGTGACAGTGGGTTTAAATCCCAAA 1200

Qy 1201 AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGGCATGAAGTTGGAATCGTAGTA 1260
Db 1201 AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGGCATGAAGTTGGAATCGTAGTA 1260
Qy 1261 ATCCGGAACAGCATGCCGCGTGAATACGTTCGCCGGCTTGTACACACGCCCGTCA 1320
Db 1261 ATCCGGAACAGCATGCCGCGTGAATACGTTCGCCGGCTTGTACACACGCCCGTCA 1320
Qy 1321 ACCATGGAGTGGTCTTACCCGACGAGCTGCGTACCTTCGGGGGCGAGGGCCAC 1380
Db 1321 ACCATGGAGTGGTCTTACCCGACGAGCTGCGTACCTTCGGGGGCGAGGGCCAC 1380
Qy 1381 GGTAGGATCAGCGACTGGGTTGAAGTCTGAACAGGTAGCGGTAGGGAACCTGCGGTG 1440
Db 1381 GGTAGGATCAGCGACTGGGTTGAAGTCTGAACAGGTAGCGGTAGGGAACCTGCGGTG 1440
Qy 1441 GATCACCCTCTT 1452
Db 1441 GATCACCCTCTT 1452

RESULT 2

US-10-049-228-2
; Sequence 2, Application US/10049228
; Publication No. US20030044886A1
; GENERAL INFORMATION:
; APPLICANT: TSUBOKURA, Akira
; TITLE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS
; FILE REFERENCE: 38331-0003
; CURRENT APPLICATION NUMBER: US/10/049,228
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/04874
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: JP 2000-175124
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA of
; OTHER INFORMATION: 81-1 strain
US-10-049-228-2

Query Match 95.0%; Score 1380; DB 14; Length 1426;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
Qy 1 AGTTTGATCTCGGTCTAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
Db 4 AGTTTGATCTCGGTCTAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 63
Qy 61 GACCTTGGGCTAGCGCGACGCGGTAGTAACGCGTGGGAGCGTCCCTCTCTACGG 120
Db 64 GACCTTGGGCTAGCGCGACGCGGTAGTAACGCGTGGGAGCGTCCCTCTCTACGG 123
Qy 121 AATAGCCCGGGAACATGGGAGTAAATACCGTATACGCCCTTTGGGGGAAGATTTATCGG 180
Db 124 AATAGCCCGGGAACATGGGAGTAAATACCGTATACGCCCTTTGGGGGAAGATTTATCGG 183
Qy 181 AGAAGGATCGCCCGCGTGGATTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGT 240
Db 184 AGAAGGATCGCCCGCGTGGATTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGT 243
Qy 241 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCAGACTC 300
Db 244 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCAGACTC 303
Qy 301 CTACGGAGGCGAGTGGGGAACTCTTAGACAATGGGGCAACCTGATCTAGCCATGCC 360

Db 304 CTACGGAGGAGCAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 363
QY 361 GCGTGAAGTATGAAGGCTTAGAGTCTTAAGCTCTTTCAGCTGGGGAAGATAATGAGCGT 420
Db 364 GCGTGAAGTATGAAGGCTTAGAGTCTTAAGCTCTTTCAGCTGGGGAAGATAATGAGCGT 423
QY 421 ACCAGCAGAAGAAGCCCGGCTAACTCCGTGCCAGCAGCCGCGGTAAATACGGAGGGGCT 480
Db 424 ACCAGCAGAAGAAGCCCGGCTAACTCCGTGCCAGCAGCCGCGGTAAATACGGAGGGGCT 483
QY 481 AGCTTTTCGGAATTAAGTGGGCTAAAGCGCAGTGAAGGCTGAAAGTCAAGAGGTG 540
Db 484 AGCTTTTCGGAATTAAGTGGGCTAAAGCGCAGTGAAGGCTGAAAGTCAAGAGGTG 543
QY 541 AATCCAGGCTCAACTTGGAACTGCTTGAACATATCAGTCTGGAGTTCGAGAGAG 600
Db 544 AATCCAGGCTCAACTTGGAACTGCTTGAACATATCAGTCTGGAGTTCGAGAGAG 603
QY 601 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGC 660
Db 604 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGC 663
QY 661 GAAGGGGCTCACTGGCTGATACGCTGAGGTGCGAAGCGTGGGAGCAACAGG 720
Db 664 GAAGGGGCTCACTGGCTGATACGCTGAGGTGCGAAGCGTGGGAGCAACAGG 723
QY 721 ATTAGATACCTGGTAGTCAAGCGCTAAAGCATGAATGCGAGAGTTCGGCAGCATGCT 780
Db 724 ATTAGATACCTGGTAGTCAAGCGCTAAAGCATGAATGCGAGAGTTCGGCAGCATGCT 783
QY 781 TGTCTGGTGTACACCTTAACGATTAAGCATTCGCTGGGAGTACGCTGCGAAGATTAA 840
Db 784 TGTCTGGTGTACACCTTAACGATTAAGCATTCGCTGGGAGTACGCTGCGAAGATTAA 843
QY 841 AACTCAAGAAATTGAGGGGGGCGCCGACAAAGCGTGGAGCATGTGTTTAATTCGAAGC 900
Db 844 AACTCAAGAAATTGAGGGGGGCGCCGACAAAGCGTGGAGCATGTGTTTAATTCGAAGC 903
QY 901 AAGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTTCT 960
Db 904 AAGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTTCT 963
QY 961 CGTAAGAGACCTGCACACAGTGTGATGGCTGTCTGACGCTGCTGCTGAGATGTC 1020
Db 964 CGTAAGAGACCTGCACACAGTGTGATGGCTGTCTGACGCTGCTGCTGAGATGTC 1023
QY 1021 GGTAAAGTCCGGCAACGAGCGCAACCCACGTCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080
Db 1024 GGTAAAGTCCGGCAACGAGCGCAACCCACGTCCTAGTTGCCAGC-ATTCAAGTTGGGCAC 1082
QY 1081 TCTATGAAACTCCCGATGATAGTGGAGGAGGTGTGATGACGTCAGTCTCTCATGG 1140
Db 1083 TCTATGAAACTCCCGATGATAGTGGAGGAGGTGTGATGACGTCAGTCTCTCATGG 1142
QY 1141 GCCTTACGGTGGGTGTACACAGTGTGTAACATGTTGTTGACAGTGGTGTAAATCCCAAA 1200
Db 1143 CCCTTACGGTGGGTGTACACAGTGTGTAACATGTTGTTGACAGTGGTGTAAATCCCAAA 1202
QY 1201 AGCCATCTCAGTTCCGATTCCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTA 1260
Db 1203 AGCCATCTCAGTTCCGATTCCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTA 1262
QY 1261 ATCGGGAACAGATGCGCGGTGAATACGTTCCGGGCGCTGTACACACCGCGCGTCAC 1320
Db 1263 ATCGGGAACAGATGCGCGGTGAATACGTTCCGGGCGCTGTACACACCGCGCGTCAC 1322
QY 1321 ACCATGGAGTGTGTTTACCGGACGAGTGGCTAAAC- -TTCGGGGGCGAGGCGGCC 1378
Db 1323 ACCATGGAGTGTGTTTACCGGACGAGTGGCTAAAC- -TTCGGGGGCGAGGCGGCC 1382
QY 1379 ACGGTAGGATCAGCGACTGGGGTGAAGTCTGTAACAAGGTAGCC 1421

Db 1383 ACGGTAGGATCAGCGACTGGGGTGAAGTCTGTAACAAGGTAGCC 1425
RESULT 3
US-09-726-774-12
; Sequence 12, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09726.774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1466
; TYPE: DNA
; ORGANISM: Bartonella henselae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1466)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-774-12

Query Match 75.3%; Score 1093.6; DB 9; Length 1466;
Best Local Similarity 87.1%; Pred. No. 1.9e-287;
Matches 1278; Conservative 0; Mismatches 161; Indels 29; Gaps 6;
QY 8 TCCTGGCTCAGAACGAGCTGGCGGAGGCTTAACACATGCAAGTCGAGGCG-AGACCTT 66
Db 1 TCCTGGCTCAGAACGAGCTGGCGGAGGCTTAACACATGCAAGTCGAGGCGACTCAT 60
QY 67 CGGCTCAGGCGGAGGCTGAGTAAAGCTGGGAGGCTGCTCTCTACGGAATAGC 126
Db 61 TAGAGTCAGCGGAGAGCGGCTGAGTAAAGCTGGGAGTCTACCTCTTCTACGGAATAGC 120
QY 127 CCGGGAACTGGGAGTAAATACCTATACGCTCTTGGGGGAAAGATTTATCGGAGAGG 186
Db 121 ACAGAGAAATTTGCTGCTAAATACCTATACGCTCTTGGGAGAAAGATTTATCGGAGAGG 180
QY 187 ATCGGCGCGGCTGGATTTAGTGTGGGTAATGGCCCAACAGCGACGATCCAT 246
Db 181 ATGAGCGCGGCTGGATTTAGTGTGGGTAATGGCTTCAACAGGCGGATCCAT 240
QY 247 AGCTGTTTGGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCTACGG 306
Db 241 AGCTGTTTGGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCTACGG 300
QY 307 GAGCAGCATGGGGAATCTTTAGACAATGGGGCAACCTGATACCCATGCGCGGTGA 366
Db 301 GAGCAGCATGGGGAATTTGGACAATGGGGCAACCTGATCCAGCCATGCGCGGTGA 360
QY 367 GTGATGAGGCTTAGGTTGTAAGCTCTTTCAGCTGGGAGATATGACGGTACCAGC 426
Db 361 GTGATGAGGCTTAGGTTGTAAGCTCTTTCAGCTGGGAGATATGACGGTAAACCGG 420
QY 427 AGAAGAGCGCGGCTAACTCCGTGCCAGCAGCGCGGTAAATACGAGGGGCTGAGGCTT 486
Db 421 AGAAGAGCGCGGCTAACTCCGTGCCAGCAGCGCGGTAAATACGAGGGGCTGAGGCTT 480
QY 487 GTTCGGAATTTACTGGCGTAAAGCGCAGTGAAGGAGTGAAGTGAAGTGAATTC 546
Db 481 GTTCGGAATTTACTGGCGTAAAGCGCATGTAGCGGATATTTAAGTCAGAGGTGAATTC 540
QY 547 CAGGGCTCAACCTTGGAACTGCTTTGAAACTATCAGTCTGAGGTTCGAGAGGCTGAGT 606
Db 541 CAGGGCTCAACCTTGGAACTGCTTTGAAACTATCAGTCTGAGGTTCGAGAGGCTGAGT 600
QY 607 GGAATCCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGGAGGC 666

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Db 601 GGAATCCGAGTGTAGAGGTAATAATCGTAGATATTCGAGGAGAACACCACTGGCGRAGGC 660
QY 667 GGCTCACTGCTGATCTAGCTGAGGTGCGAAGCGTGGGAGAGCAACACAGATTAGA 726
Db 661 GGCTCACTGCTGATCTAGCTGAGGTGCGAAGCGTGGGAGAGCAACACAGATTAGA 720
QY 727 TACCTCTGATGTACAGCGCTTAACGATGAATCCAGACCTGCGCAGCATGCTTCTCGG 786
Db 721 TACCTCTGATGTACAGCGCTTAACGATGAATGTAGCCGTTGGGTGGTTTACTGTCTAG 780
QY 787 TGTCAACCTTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGAT 846
Db 781 TGGCGCAGCTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGAT 840
QY 847 AAGGAATTAACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 906
Db 841 AAGGAATTAACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
QY 907 CAGAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCTTACCA 962
Db 901 CAGAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCTTACCA 960
QY 963 TAAGAGACCTGCACACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1022
Db 961 CGGCTGATCGGAGACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1023 TTAAGTCCGCGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1082
Db 1021 TTAAGTCCGCGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1079
QY 1083 TATGGAACCTGCGGATGATAAGTCG-GAGGAAGGTGTGGATGACGTCAAGTCTCATGGG 1141
Db 1080 TAGGGGACCTGCGGATGATAAGTCG-GAGGAAGGTGTGGATGACGTCAAGTCTCATGG 1139
QY 1142 CTTACGGGTGGGCTACACAGCTGCTTACAAATGGTGGTACAGTGG----- 1187
Db 1140 CTTACGGGTGGGCTACACAGCTGCTTACAAATGGTGGTACAGTGG----- 1199
QY 1188 -----GTTAAATCCCAAGGCACTCTAGTTCGATGCTGCTGCTGCTGCTGCTGCTG 1240
Db 1200 AGTCTGAGCTAAATCTCCAAAGGCACTCTAGTTCGATGCTGCTGCTGCTGCTGCTG 1259
QY 1241 TGAAGTTGGAATCGCTAGTAAATCGCGAAGCAGCATGCGGCGTGAATACGTTCCCTGCA 1300
Db 1260 TGAAGTTGGAATCGCTAGTAAATCGCGAAGCAGCATGCGGCGTGAATACGTTCCCTG 1319
QY 1301 TTGTACACCGCGGCTGACACCATGGAGTGGTCTACCCGACGACGNTGCGCTAAC 1360
Db 1320 TTGTACACCGCGGCTGACACCATGGAGTGGTCTACCCGACGACGNTGCGCTAAC 1379
QY 1361 TTGGGGGGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1420
Db 1380 GCAAGGAGCGAGTACCAACCGGTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGG 1439
QY 1421 CGTAGGGGAACCTGCGGCGTGGATCACT 1448
Db 1440 CGTA-GGGAACCTGCGGCTGGATCACT 1466
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RESULT 4

US-09-894-467-2/c
; Sequence 2, Application US/09894467
; Patent No. US2002015519A1
; GENERAL INFORMATION:
; APPLICANT: Lindner, Luther E.
; APPLICANT: Macphree, Kathleen
; TITLE OF INVENTION: Human Blood Bacterium
; FILE REFERENCE: D6026D
; CURRENT APPLICATION NUMBER: US/09/894,467
; PRIORITY FILING DATE: 2001-06-28
; PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 2
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: 58 rRNA sequence of a new human blood bacterium
US-09-894-467-2

Query Match 74.88; Score 1086.4; DB 10; Length 1502;
Best Local Similarity 86.28; Pred. No. 1.7e-285;
Matches 1245; Conservative 0; Mismatches 177; Indels 23; Gaps 3;

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QY 20 ACNAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCGGC 79
Db 1502 ACNAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCGGC 1443
QY 80 GGACGGGTGAGTAACGCGTGGGAACGTCCTCTACGGAATAGCCCGGGGAACTGG 139
Db 1442 GGACGGGTGAGTAACGCGTGGGAACGTCCTCTACGGAATAGCCCTGGGAACTAG 1383
QY 140 GAGTAATACGTAATACGCCCTTTGGGGAAAGATTATTCGGAAGAGATCGGCCCGGCTT 199
Db 1382 GGCTAATACCGGATACGCCCTTTATGGGAAAGGTTTACTGCGGAAGATCGGCCCGGCTC 1323
QY 200 GATATTAGGTAGTTGGTGGGTAATGCGCCACCAAGCGCAGCATCATAGCTGGTTGAGA 259
Db 1322 TGATTAGTATGTTGGTGGGTAACGGCTTACCAAGGCGCAGCATCAGTAGCTGGTCTGAGA 1263
QY 260 GGATGATACGCCACACTGGGACTGAGACAGCGGCCAGACTCCTACGGGAGGACGACAGTGG 319
Db 1262 GGATGATACGCCACACTGGGACTGAGACAGCGGCCAGACTCCTACGGGAGGACGACAGTGG 1203
QY 320 GGAATCTTAAACAATGGGGCAACCTGATCTAGCCATAGCCGCTGAGTATGATGAAGGCT 379
Db 1202 GGAATATTGACAATGGGGCAACCTGATCTAGCCATAGCCGCTGAGTATGATGAAGGCT 1143
QY 380 TAGGGTGTAAAGCTCTTTTCAGCTGGGAAGATATGAGTACGCTACGAGCAGAGAGAGCCCG 439
Db 1142 TAGGGTGTAAAGCTCTTTTCAGCTGGGAAGATATGAGTACGCTACGAGCAGAGAGAGCCCG 1083
QY 440 GCTAACTCCGTGCGCAGCAGCGGCTAATACGGAGGGGCTAGCGTTGTCGGAATTA 499
Db 1082 GCTAACTCCGTGCGCAGCAGCGGCTAATACGGAGGGGCTAGCGTTGTCGGAATTA 1023
QY 500 GGCGCTAAAGCGCAGCTAGCGGAGCTGGAAGTCAGAGGTGAATCCACGGGCTCACT 559
Db 1022 GGCGCTAAAGCGCAGCTAGCGGAGCTGGAAGTCAGAGGTGAATCCACGGGCTCACT 963
QY 560 TGAACCTGCCTTTGAAACTATCAGTCTGAGGTTCGAGAGAGGTGAGTGGATTCGGAGTG 619
Db 962 CAGATGGCTCTCGATCTAGCTGAGGTTCGAGAGAGGTGAGTGGATTCGGAGTG 903
QY 620 TAGAGTGAATTCGATAGATTTTCGGAGGAAACCACTGCGGAGGCGGCTCACTGGCTC 679
Db 902 TAGAGTGAATTCGATAGATTTTCGGAAGAACACCGGTGCGGAAGGCGGCACTGGAGCC 843
QY 680 GATACCTGAGCTGAGGTGCGAAGCGTGGGAGCAACAGGATTAGATACCTCGTGTAGTC 739
Db 842 ATTACTGAGCTGAGGCGCGGAGGCAACAGGATTAGATACCTCGTGTAGTC 783
QY 740 CAGCGCTAAACGATGAATCCAGAGCTGCGGAGGATGCTTGTGCTGTGCACACTAAC 799
Db 782 CAGCGCTAAACGATGAATCCAGAGCTGCTTGGGTGCTTGCACCGCAGTACGCGAGCTAAC 723
QY 800 GATTAAAGCATTCGCGCTGGGAGTACGCTGCGAAGATTAAACTCAAGGAATGACGG 859
Db 722 GCTTTGAGCATTCGCGCTGGGAGTACGCTGCGAAGATTAAACTCAAGGAATGACGG 663
QY 860 GGCGCCGCGACAGCGGTGGAGCATGTGTTTAAATTCGAACACAGCGGCGCAGACTTACCA 919
Db 662 GGCGCCGCGACAGCGGTGGAGCATGTGTTTAAATTCGAACACAGCGGCGCAGACTTACCA 603
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[illegible]

RESULT 7

US-09-902-693-1
; Sequence 1, Application US/09902693
; Patent No. US20020061561A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: TAKEUCHI, Sonoko
; APPLICANT: TOJIMA, Yasuko
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: FUDOU, Ryosuke
; APPLICANT: YOKOZEKI, Kenzo
; TITLE OF INVENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR
; TITLE OF INVENTION: D-XYLULOSE

960	AAAGGGGCGACCTGGAGCAAAATCCCGAAAAACCGTCTCAGTTGCGATTGCATCTGCACACT	1019
1233	CGAGGGCATGAACTTGGAAATCGCTAGTAAATCGCGGAACAGCATCCGCGGGTGAATACGTT	1292
1020	CGGGTGCATGAAGGCGGGAATCGCTAGTAAATCGTGGATCAGCATGCCAGGTGAATACGTT	1079
1293	CCCGGGCCTTGTACACACCGCGGTCACACCATGGGAGTTTGGTTCTACCCGACACGACGNWG	1352
1080	CCCGGGCCTTGTACACACCGCGGCTCACACCATGGGAGTTGGCTTACCCGACCGGCGCTG	1139
1353	CGCTAACCTTCGGGGGGCAGCGGGCCACGGTAGATCATAGCGACTGGGGTGAAGTCGTAAAC	1412
1140	CGCCAAACCGAAGGAGGCGAGCGACCGGTAGGGTCAGCGACTGGGGTGAAGTCGTAAAC	1199
1413	AAAGGTAGCC	1421
1200	AAAGGTAGCC	1208

RESULT 9

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US-09-847-513A-1
; Sequence 1, Application US/09847513A-
; Publication No. US20030104375A1
; GENERAL INFORMATION:
; APPLICANT: MBARI
; APPLICANT: DeLong, Edward
; APPLICANT: Beja, Oded
; TITLE OF INVENTION: Light-driven energy generation using proteorhodopsin
; FILE REFERENCE: MBA-101
; CURRENT APPLICATION NUMBER: US/09/847,513A
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/201,602
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 105184
; TYPE: DNA
; ORGANISM: Naturally occurring gamma proteobacterium
; FEATURE:
; NAME/KEY: gene
; LOCATION: (50866)..(51615)
; OTHER INFORMATION: Proteorhodopsin gene sequence.
; NAME/KEY: misc_feature
; LOCATION: (1593)..(2807)
; OTHER INFORMATION: Predicted threonine dehydratase. Contains 'n' at position 2753.
; PUBLICATION INFORMATION:
; AUTHORS: Beja, O., Aravind L., Koonin, E.V., Suzuki, M.T., Hadd, A., Nguyen, L.P.,
; AUTHORS: Jovanovich, S.B., Gates, C.M., Feldman, R.A., DeLong, E.F.
; TITLE: Bacterial rhodopsin: evidence for a new type of phototrophy in the sea
; JOURNAL: Science
; VOLUME: 289
; ISSUE: 5486
; PAGES: 1902-1906
; DATE: 2000-09-15
; DATABASE ACCESSION NUMBER: AF279106
; DATABASE ENTRY DATE: 2000-06-15
; RELEVANT RESIDUES: (50866)..(51615)
US-09-847-513A-1

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QY	110	CTTCTCTACGGAATAGCCCCGGGAACATGGGGAGTAAATACCGGTATACGCCCTTTGGGGGAA	169
Db	97785	TAGTAGAAGGGATAGCCCGGGGAAACCCGGATTAATACCGGTATACCTCCTTCGGGAGAA	97844
QY	170	AG-----ATTTATCGGAGNAGGATCGGCCGGTGGGATAGGTAGTGG	214
Db	97845	AGAAGCCCTCTCTTTGAAGCTTTTCGTACTAGATGAGCCTCGGTAAAGATTAGCTTGTGG	97904
QY	215	TGGGTTAATGGCCCAACAGCGAGATCCATAGCTTGTTCGAGAGGATGATCAGCCACA	274
Db	97905	TGAGGTTAAGGCTCACCAGGCGAGATCTTTAGCTGTCTGAGAGGAGCATCAGCCACA	97964
QY	275	CTGGGACTGAGACAGCGGCCAGACTCCTACCGGAGGAGCAGCAGTGGGGAATCTTAGACAAT	334
Db	97965	TTGGGACTGAGACAGCGGCCAGACTCCTAAGGGAGGAGCAGCAGTGGGGAATATTGGACAAT	98024
QY	335	GGGGCAACCCCTGATCTAGCCATCGCGCTGAGTGTGAAGCCCTTAGGGTTGTTAAAGCT	394
Db	98025	GGGCGCAGCCCTGATCCAGCCATACCGCTGTGTGAAGAAGGCCCTTCGGGTTGTAAAGCA	98084
QY	395	CTTTCAGCTGGGAAGATAA-----TGAGGTTACCAAGCAGA	429
Db	98085	CTTTAGCAGGAGNGAAAAAGTTATAGTTAATACCTTATAACCTTGATGTACCTGCAGA	98144
QY	430	AGAAAGCCCGGCTAACTCCGTGCCAGCAGCCCGGTAAATACGGAGGGGGCTAGCGTTGTT	489
Db	98145	ATAAGCACCGGCTAATTCGTGCCAGCAGCCCGGTAAATACGGAAGGTCAAGCGTTAAT	98204
QY	490	CGGAATTACTGGCGTAAAGCGCAGTAGGCGGACTGGAAGACTCAGAGGTGAAATCCGAG	549
Db	98205	CGGAATTACTGGCGGTAAAGCGCGGTAGTGTGTTAAGTTGGATGTGAAAGCCCTG	98264
QY	550	GGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCCAGAGAGGTGAGTGA	609
Db	98265	GGCTCAACCTAGAACTGATCCAAACTTAATCTACTAGGTACCATAGAGGAGGTAGA	98324
QY	610	ATTCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAAACACAGTGGCGAAGCGCGC	669
Db	98325	ATTCAATAGTGTAGCGTGGAAATCGGTAGATATTATGAAGAATACCAATGGCGAAGCGCGC	98384
QY	670	TCACTGGCTCGATCTAGCAGCTGAGGTGCGAAAGGTGGGGAGCAACAGGATTAAGATAC	729
Db	98385	CTCCTGGATCTGTACTTGACACTGAGGTGCGAAAGGTGGGTAGCGAACAGGATTAAGATAC	98444
QY	730	CCTGGTAGTCCAGCGGTAAACGATGAATGCCAGACGTGGCA-AGCATGCTTGTCGGTG	788
Db	98445	CTGGTAGTCCAGCGGTAAACGATGAATGAACATAGCAACTAGCTGTGGGAGACTATGCTTTCAGTG	98504
QY	789	TCACACCTAACGGATTAAGCATTCGCCCTGGGAGTACGTCGCAAGATTATAAAGTCAAA	848
Db	98505	GCAGACCTAACGCTTTAAGTTGTCGCCCTGGGAGTACGCGCGCAAGGCTAAAGTCAAA	98564
QY	849	GGAAATTGACGGGGCCGCACAAAGCGGTGGAGCATGTGTTTAAATTCGAAGCAAGCGCA	908
Db	98565	TGAATTTGACGGGGACCCGCACAAGCGGTGGAGCATGTGTTTAAATTCGATGCAAGCGCAA	98624
QY	909	GAACCTTTACCAACCCCTTGACATGGCAAGCCGCTGGAGAGATTACGCTTTCTCGTAAGAG	968
Db	98625	AAACCTTACCTACTCTTGACATCACTTGGAG-GGCTCTTGAATGAGAGGTGTCCTTTTGA	98683
QY	969	ACCTGCACACAGGTGCTGATGGCTGTCTGCAGCTCGTGTGCTGAGATGTTTCGGTTAAGT	1028
Db	98684	ACCAAGATACAGGTGCTGATGGCTGTCTGCAGCTCGTGTGCTGAGATGTTTCGGTTAAGT	98743
QY	1029	CGGGCAACGAGCGCAACCCAGTCCTTAGTTGCCAGCAATTCAGTTGGGAACCTCTATGGA	1088
Db	98744	CGGATAACGAGCGCAACCCCTTACCCTTATTTCGCAGCATTCGGTCGGGAACTATAAGGG	98803
QY	1089	AACTGCCGATGATAAGTCGGAGGAAGGTGTGATGACGTCAAGTCTCATGGCCCTTACG	1148
Db	98804	GACTGCCGCTGATAAACCCGGAGGAGGTGAGGACGACGTCAAGTCAATCATGCGCCTTACG	98863
QY	1149	GGTTGGGCTACACACCGTGTACAATGGTGGTGACAGTGG-----1188	

Db. 98864 AGTAGGCTACACAGCTGCTACAAATGGAGATACAGACGCGTAAGCCGCGAGGTGGT 98923
Qy 1189 --TTAATCCCAAAAGCCATCTCAGTTTCGGATTGCTCTGCAACTGCGAGGGCATGAAGT 1246
Db 98924 GCTAATCCTAAAGATCTTTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGT 98983
Qy 1247 TGGATCGCTAGTAATCGCGGACAGCATGCGCGGTGTAATAGTTCCCGGGCTTGTAC 1306
Db 98984 CGGAATCGCTAGTAATCGCGGATCAGCATCCGCGGTGAATAGCTTCTCGGGCTTGTAC 99043
Qy 1307 ACACGCGCGCTCACACATGGAGTTGTTCTACCCGACGAGTGGCTAACTTCGGG 1366
Db 99044 ACACGCGCGCTCACACATGGAGTTGTTCTACCCGACGAGTGGCTAACTTCGGG 99103
Qy 1367 GGGCAGCGCGCAGCTAGGATGAGTGGGCTGAAGTCTGTAACAGGTAGCGGTAGG 1426
Db 99104 AGGCGGTTTACCAGGTTGCTTCTCATGCTGAGTGGGTGAAGTCGTAACAGGTAGCGGTAGG 99163
Qy 1427 GGAACCTGGCGTGGATCACTCGTT 1452
Db 99164 GGAACCTGGCGTGGATCACTCGTT 99189

RESULT 10

US-10-007-725-6
; Sequence 6, Application US/10007725
; Publication No. US20020150887A1
; GENERAL INFORMATION:
; APPLICANT: Maruyama, Akihiko
; APPLICANT: Higashihara, Takanori
; APPLICANT: Kitamura, Keiko
; APPLICANT: Sunamura, Michinari
; APPLICANT: Kurane, Ryuchiro
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID PROBES FOR
; TITLE OF INVENTION: MOLECULAR GENETIC ANALYSIS OF POLLUTED ENVIRONMENTS AND
; FILE REFERENCE: 13558-003001
; CURRENT APPLICATION NUMBER: US/10/007,725
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: JP 341765/2000
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Cycloclasticus pugetii
US-10-007-725-6

Query Match 59.9%; Score 869.8; DB 13; Length 1532;
Best Local Similarity 76.7%; Pred. No. 1.3e-226;
Matches 1175; Conservative 1; Mismatches 274; Indels 82; Gaps 6;

Qy 1 AGTTGATCTCGGCTCAGACGACGCTGCGCGGAGCTTAACACATGCAAGTCGAGCGA 60
Db 3 AGTTGATCATGGCTCAGATTGAACGCTGGCGGATGCTTAAACATGCAAGTCGAGCGG 62
Qy 61 GACCTTCG-----GGTCTAGCGCGGAGCGGTGAGTGGCGGAGTGAAGTCGAGG 102
Db 63 AACAGATGCGAGCTTGTAGCAGCGGTGAGTGGCGGAGCGGTGAGTGAAGTAGGA 122
Qy 103 ACGTGCGCTTCTACGGAATAGCCCGGAACTGGGAGTAATACCGTATACCGCTTT 162
Db 123 ATCCGCGCGATGAGTGGGGGACAACTCTCTGAACAGCTGCTTAATACCGCATATCCCGCG 182
Qy 163 GGGGGAAGA-----TTTATCGGAGAGATCGCGCGCGGTGGATTAGGT 208
Db 183 GGGGCAAGAGACGGGACCTTCGGGCTTCTAATGGATGAGCTACAGGGGATTAGGT 242
Qy 209 AGTTGGTGGGTAAATGGCCCAAGCGGAGCTTCAATAGCTGTTTGGAGAGGATGATCA 268
Db 243 AGTTGGTGGGTAAACGGCTCACCAGGCAACATCCCTAGCTGTTTGGAGAGGATGATCA 302

Qy 269 GCCACACTGGGACTGAGACACGCCCCAGACTCTCTACGGAGGAGCAGAGTGGGAACTCTTA 328
Db 303 GCCACACTGGGACTGAGACACGCCCCAGACTCTCTACGGAGGAGCAGAGTGGGAACTCTTA 362
Qy 329 GACAATGGGGGCAACCTGATCAGCCATCGCGGTGAGTGAAGGCCCTTACGGGTGT 388
Db 363 CACAATGGGAGAACTCTGATGAGCAATCGCGGTGAGTGAAGGCCCTTACGGGTGT 422
Qy 389 AAAGCTCTTTCAGGTGGGAGATAA-----TGACGGTAC 422
Db 423 AAAGCTCTTTCAGGTGGGAGATAA-----TGACGGTAC 482
Qy 423 CAGCAGAAAGAGCCCGCTTAACCTCGTCCAGCAGCGCGGTATACGGAGGGGGCTAG 482
Db 483 CTACAGAAAGAGCAGCCGCTTAACCTCGTCCAGCAGCGCGGTATACGGAGGGGGCTAG 542
Qy 483 CGTTGTTCCGAATTTACTGGCGTAAAGCGCAGTGGCGGACTGGAAGTCTCAGAGGTGAA 542
Db 543 CGTTAATCGGAATTTACTGGCGTAAAGCGCGCAGCGGGTTAAACAAGTCAGATGTGAA 602
Qy 543 ATCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTCGAGGTTCGAGAGGT 602
Db 603 AGCCCGGGCTCAACCTTGGAACTGCCTTTGAAACTAGCTAGATGTGTTAGAGGA 662
Qy 603 GAGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGACACACAGTGGCGA 662
Db 663 GAGTGGAAATTCAGTGTAGCGTGAATTCGTAGATATTCGAGGAAACACACAGTGGCGA 722
Qy 663 AGCGCGCTACTGGCTCGATCACTGAGTGGCGGAGTGGCGGAGCAACAGGAT 722
Db 723 AGCGCGCTCTCTGGACCAACACTGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGG 782
Qy 723 TAGATACCTGCTAGTCCACCGCTTAACAGTGAATGCGCAGACGCTCGCAACAGTCTGTG 782
Db 783 TAGATACCTGCTAGTCCACCGCTTAACAGTGAATGCGCAGACGCTCGCAACAGTCTGTG 842
Qy 783 TCGGTGTCACTACCTTAACGATTAAGCTTCGCGCTGGGAGTACGGTGGCGAAGTATATA 842
Db 843 TTAGTGGTGCA-STACGCAATAGTTGACCGCTGGGAGTACGGCGGAGGCTGAGGCTATA 901
Qy 843 CTCAAGGATTTGACGGGGCGCCACAGCGGTGGAGCATGTGTTTAAATTCGAGCA 902
Db 902 CTCAATGAATGACGGGGCGCCACAGCGGTGGAGCATGTGTTTAAATTCGAGCA 961
Qy 903 CGCGCAGAACCTTACCAACCTTGCATGGCAGGACCGCTGGAGAGATTCAGTCTTCG 962
Db 962 CGCGAAGAACCTTACCAACCTTGCATGGCAGGACCGCTGGAGAGATTCAGTCTTCG 1021
Qy 963 TAAGAGACTGCACACAGGCTGCTGATGGCTGCTGATGCTGCTGATGATGCTGCG 1022
Db 1022 TCGGAACTCTGTATACAGGCTGCTGATGGCTGCTGATGCTGCTGATGATGCTGCG 1081
Qy 1023 TTAAGTCCGCAACGAGCGCAACCGCTGCTGATGGCTGCTGATGCTGCTGATGATGCTG 1082
Db 1082 TTAAGTCCGCAACGAGCGCAACCGCTTATCTCTAGTGTCTA-CCATTAGTGGGACTC 1140
Qy 1083 TATGGAACCTGCCGATGATAGTGGAGGAGGTGTGGATGACGCTCAAGTCTCATGCGC 1142
Db 1141 TAAGGAGACTGCCGCTGATTAACCGGAGGAGGTGGGAGCAGCTCAAGTCTCATGCGC 1200
Qy 1143 CTTAGCGGTGGGCTACACAGCTGCTACATGTTGGTGGTGCAGTGGG----- 1188
Db 1201 CTTAGGTTAGGCTACACAGCTGCTACATGTTGGGCTGACAGAGGCGCGCAACCTCGCGA 1260
Qy 1189 -----TTAATCCCAAAAGCCATCTCAGTGGATTGCTCTGCAACTCGAGGCA 1240
Db 1261 GAGTAAGCTAATCCTTAAAGCCGCTCTAGTCCGATTTGAGTCTGCACTCGACTGCA 1320
Qy 1241 TGAAGTGGAAATCTAGTAAATCGCGGAACAGCATGCCCGGTGAATACGTTCCCGGCGC 1300
Db 1321 TGAAGTGGAAATCTAGTAAATCGCGGAACAGCATGCCCGGTGAATACGTTCCCGGCGC 1380

QY 1301 TTGTACACACCGCCGCTCACACCATGGAGTGTCTTACCCGACGAGNCGCTACCC 1360
DB 1381 TTGTACACACCGCCGCTCACACCATGGAGTGTCTTACCCGACGAGNCGCTACCC 1440
QY 1361 TTCGGGGGAGCGGCCGACCGTGGAGTACGACGACTGGGGTGAAGTTCGTAACAAGGTAGC 1420
DB 1441 TTCGGGGGAGCGGCCGACCGTGGAGTACGACGACTGGGGTGAAGTTCGTAACAAGGTAGC 1500
QY 1421 CTTAGGGGAACCTCGCGCTGGATCACCTCCTT 1452
DB 1501 CCTAGGGGAACCTCGCGCTGGATCACCTCCTT 1532

RESULT 11
US-10-007-725-5
; Sequence 5, Application US/10007725
; Publication No. US20020150887A1
; GENERAL INFORMATION:
; APPLICANT: Maruyama, Akibiko
; APPLICANT: Higashihara, Takanori
; APPLICANT: Kitamura, Keiko
; APPLICANT: Sunamura, Michinari
; APPLICANT: Kuzane, Ryuchiro
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID PROBES FOR
; TITLE OF INVENTION: MOLECULAR GENETIC ANALYSIS OF POLLUTED ENVIRONMENTS AND
; TITLE OF INVENTION: ENVIRONMENTAL SAMPLES
; FILE REFERENCE: 13558-003001
; CURRENT APPLICATION NUMBER: US/10/007,725
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: JP 341765/2000
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: GR211-P1(FERM P-17394)
US-10-007-725-5

Query Match 59.5%; Score 863.4; DB 13; Length 1494;
Best Local Similarity 77.4%; Pred. No. 7.1e-225;
Matches 1157; Conservative 0; Mismatches 257; Indels 80; Gaps 6;

QY 5 TGATCTGCTCAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTTCGAGCGAGACC 64
DB 1 TTATCATGGCTCAGATTGAACGCTGGCGGACGCTTAACACATGCAAGTTCGAGCGAAAC 60
QY 65 TTC-----GGGTCTAGCGGGGACGGGTGAGTAAACGGTGGGACGTGC 108
DB 61 GATCCTAGCTGTAGGAGCGCTCGAGCGGGGAGGTGAGTAAACGCTGAGAACTCTGC 120
QY 109 CCTTCTCTACGGATAGCCCGGAAACTGGAGTAACTACCGTATACCGCCCTTTGGGGGA 168
DB 121 CCATTAGGGGATACCTTGGGAAACCCAGGCTAATACCGCATATCCCTACGGGGGA 180
QY 169 AA-----GATTATCGGAGAGAGTATGGCCCGCTGGTGGATTAGGTAGTGG 214
DB 181 AAGCAGGGGATCTTCGGACCTTGTGCTGATGGATGAGTCTCGCTCGGATTAGCTTTGG 240
QY 215 TGGGGTAAATGGCCACCAACCGGACGATCCATAGCTGGTTGAGAGATGATACGCCACA 274
DB 241 TGAGGTAAATGGCTCACCAGGCGACGATCCGCTAGCTGGTCTTAGAGATGATACGCCACA 300
QY 275 CTGGGACTGAGACAGCGCCAGACTCCTACGGGAGGACGAGTGGGGAATCTTAGACAAT 334
DB 301 CCGGGACTGAGACAGCGCCAGACTCCTACGGGAGGACGAGTGGGGAATCTTAGACAAT 360
QY 335 GGGGGCAACCTGTATAGCATGCCCGCTGAGTGAAGGCGCTTAGGGTTGTAAGCT 394
DB 361 GGGGGCAACCTGTATAGCATGCCCGCTGAGTGAAGGCGCTTAGGGTTGTAAGCA 420

QY 395 CTTTCAGCTGGGAAGATAA-----TGACGGTACCAGCAGA 429
DB 421 CTTTCAGTGGGAGGAAGGCTTATCCTTAATACGGATGAGTACTTTGAGCTTACCTACAGA 480
QY 430 AGAAGCCCCGGCTAACTCCGTGCCAGCAGCCGGTAAATACGGAGGGGGCTAGCGCTTGT 489
DB 481 AGAAGCACCGGCTAATTTTCGTGCCAGCAGCCGGTAAATACGAAAGGTGCGAGCCTAAT 540
QY 490 CGGAATTAATCGGGCTAAAGCGCAGCTAGCGGAGTGGAAAGTCAAGAGTGAATATCCAG 549
DB 541 CGGAATTAATCGGGCTAAAGCGGCTAGCGGCTTGTCTAAGTCAAGTGTGAAGACCCCG 600
QY 550 GGCCTAACCTTGGAACTGCTTGAACATATCAGTCTGAGTTCGAGAGAGGTGAGTGA 609
DB 601 GGCCTAACCTTGGAACTGCTTGAACATGCGAGGCTAGATGCAATGAGGAGGTGGA 660
QY 610 ATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGAGAGGACACACAGTGGGGAAGCGCGC 669
DB 661 ATTCGCGGTGTAGCGGTGAAATGCTAGAGATCGGAAGAACACACAGTGGGGAAGCGCGC 720
QY 670 TCACTGGCTCGATTAATGAGCTGAGGTGCGAAAGCGTGGGAGGACAAAGAGATTAGATAC 729
DB 721 CTCCTGGACTGACATTTGAGCTGAGGTGCGAAAGCGTGGGAGGACAAAGAGATTAGATAC 780
QY 730 CCTGTAGTCCACCGCTAAAGCATGATGCGAGACGTCGCGAAGC--ATGCTTCTCGT 787
DB 781 CCTGTAGTCCACCGCTAAAGCATGCTACTAGTCTGTTGGGAATCTTAGTATTCTTGGT 840
QY 788 GTCACACCTAACCGATTAAAGCATTCGCGCTGGGAGTACGCTGCGAAGATTAAAACTCAA 847
DB 841 GACGAGTTAAAGCATTAAGTAGACCGCTGGGAGTACGCGGAGGTTAAACTCAA 900
QY 848 AGGAATTGACGGGGCGCGCACAGCGTGGAGCATGTGGTTTAAATTCGAAGCAACGCGC 907
DB 901 ATGAATTGACGGGGCGCGCACAGCGTGGAGCATGTGGTTTAAATTCGATGCAACGCGA 960
QY 908 AGAACCTTACCACCCCTTGACATGGCAGGACCGTGGAGAGATTCAGCTTCTCCTAAGA 967
DB 961 AGAACCTTACCAGGCTTGCATCCTTGGAACTTCTAGAGATAGATTGGTGCCTTCGGG 1020
QY 968 GACCTGCACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1027
DB 1021 AGCCAAAGTACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1028 TCCGGCAACGAGCGCAACCCAGTCCCTAGTGTGCGAGCAATTCATCA--GTTGGGAACCTCTATG 1086
DB 1081 TCCGGTAAACGAGCGCAACCCCTTGTCCCTAGTGTGCGAGCAGCTAATGTTGGGAACCTCTAGG 1140
QY 1087 GAAACTGCCGATGATAAGTCCGAGGAGGTGTTGATGACGTCAAGTCTCCTATGGGCCCTTA 1146
DB 1141 GAGACTGCCGCTGACAAACCGGAGGAGGTGGGAGACGCTCAAGTCAATCATATGCGCCCTTA 1200
QY 1147 CGGGTGGGCTTACACACGCTGTACAAATGGTGGTGCAGCTGGG----- 1188
DB 1201 CGGCTGGGCTTACACACGCTGTACAAATGGGAGTACAGAGGACGCAAAAGTCCGAGGCC 1260
QY 1189 -----TTAATCCCCAAAAGCCATCTCAGTTCGGATTGCTCTGCAACCTCGAGGCGATGAA 1244
DB 1261 AAGCAAAATCCCTTAAACTGTTCCGTAGTTCGGATTGGAGTCTGCAACCTCGACTCCATGAA 1320
QY 1245 GTTGGAAATCGTAGTAATCGCGGACACATGCGCGGTGAGTACGTTCCCGGGGCTTGT 1304
DB 1321 GTCGGAATCGTAGTAATCGCGGATCAGAAATGCGCGGTGAGTACGTTCCCGGGGCTTGT 1380
QY 1305 ACACACCGCGCTCACACATGGGAGTGTGTTCTTACCGGACGACGCTGCGTAACTTCG 1364
DB 1381 ACACACCGCGCTCACACATGGGAGTGTGTTCTTACCGAGAGTGTGATAGTCTTAACTTCG 1440
QY 1365 GGGGCGAGCGGCCACGCTAGGATCAGCGACTGGGGTGAAGTCTGTAACAAGSTA 1418
DB 1441 GGAGGAGCTTCACACCGGTGTGTTTCATGACTGGGGTGAAGTCTGTAACAAGSTA 1494

Db 662 TGCGTAGATATAGGAAGAACACACAGTGGCGAAGCGGACCCTGGACTGATACGAC 721
Qy 691 TGAGTCCGAAAGCGTGGGAGCAACACAGATAGATACCTGTGTCTCCACGCCGTAAA 750
Db 722 TGAGTCCGAAAGCGTGGGAGCAACACAGATAGATACCTGTGTCTCCACGCCGTAAA 781
Qy 751 CGATGAATGCCAGACGTCGGCAAGCATGCT-TGTCGGTGTACACCTAACGGATTAAACA 809
Db 782 CGATGCAACTAGCCGTGGAGCCCTTGACCTCTTAGTGGCGACGTAACGCATTAAGTT 841
Qy 840 TTCGCGCTGGGAGTACGGTCGCAAGATTAAACTCAAAGGAATTGACGGGGCCCGCAC 869
Db 842 GACCGCTGGGAGTACGGTCGCAAGGTAAACTCAAAGGAATTGACGGGGCCCGCAC 901
Qy 870 AAGCGGTGGAGCATGTGGTTTAATCGAAGCAAGCGCAGAACCTTACCACCCCTTGACA 929
Db 902 AAGCGGTGGAGCATGTGGTTTAATCGAAGCAAGCGCAGAACCTTACCAGGCTTGACA 961
Qy 930 TGGCAGGACCGCTGGAGAGATTACGCTTCTCGTAAGAGACCTGCACACAGGTGCTGCAT 989
Db 962 TCCAAATGAACCTCCAGAGATGGATGGGTGCGCTTCGGGAACATTTGAGACAGGTGCTGCAT 1021
Qy 990 GGCTGTGCTCAGCTCGTGTGAGATGTTTGGTTAAAGTCCGGCAAGCGGCAACCCAC 1049
Db 1022 GGCTGTGCTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGTAACGAGCGCAACCCCT 1081
Qy 1050 GTCCCTAGTTGCCAGCAATCA-GTTGGGAACCTATGGAACCTGCCGATGATAAGTCGG 1108
Db 1082 GTCCCTAGTTACCAGCACGTAATGTTGGGCACTCTAAGGAGACTGCCGGTGACAACCGG 1141
Qy 1109 AGGAAGTGTGGATGACGTCAAGTCCTCATGGGCGCTTACGGGTTGGGCTACACACGTGCT 1168
Db 1142 AGGAAGTGTGGATGACGTCAAGTCCTCATGGGCGCTTACGGGCTGGGCTACACACGTGCT 1201
Qy 1169 ACAATGTTGTGACAGTGGGT-----AATCCCCAAAAGCCAT 1206
Db 1202 ACAATGTTGTGACAGAGGTGGCAAGCGCGAGGTGGAGCTAATCCCAAAACCGAT 1261
Qy 1207 CTCAGTTCCGATTGCTCTGCAACTCGAGGCAATGAAGTTGGATCGCTAGTAATCGCG 1266
Db 1262 CGTAGTCCGATCGCAGTCTGCAACTCGACTCGCTGAAGTCGGAATCGCTAGTAATCGCG 1321
Qy 1267 GAACAGCATGCCGGGTGAATACGTTCCGGGCGCTTGTACACACCGCCCGTCACACCATG 1326
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Qy 1327 GGAGTGTGTTCTACCCGACGACGNTGCGCTAACCTTCGGGGGCGAGCGGCCACGCTAGG 1386
Db 1382 GGAGTGTGTTGACCAAGATAGCTAGTCTAACCTTCGGGAGGACGGTTACCAACGGGTG 1441
Qy 1387 ATCAGCGACTGGGTGAAGTCGTAACAAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1446
Db 1442 ATTCATGACTGGGTGAAGTCGTAACAAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501

Search completed: July 28, 2003, 13:02:01
Job time : 367 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 09:18:54 ; Search time 4119 Seconds
(without alignments)
11551.083 Million cell updates/sec

Title: US-10-049-228-1

Perfect score: 1452

Sequence: 1 agttgatctgctgcagaa.....tgogctggatcacctcctt 1452

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pna/US06_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1451	99.9	1452	35	US-09-856-640-1
2	1451	99.9	1452	44	US-10-049-228-1
3	1380	95.0	1426	44	US-10-049-228-2
4	1285.2	88.5	1404	47	US-10-166-225A-12

5	1285.2	88.5	1404	84	US-60-296-299-12	Sequence 12, Appl
6	1212.6	83.5	1385	32	US-09-735-567-1	Sequence 1, Appl
7	1212.6	83.5	1385	71	US-60-171-140-1	Sequence 1, Appl
8	1113	76.7	20310	32	US-09-739-449-191	Sequence 191, App
9	1113	76.7	20310	34	US-09-803-110-191	Sequence 191, App
10	1093.6	75.3	1466	32	US-09-726-774-12	Sequence 12, Appl
11	1086.4	74.8	1502	1	PCT-US98-23674-2	Sequence 2, Appl
12	1086.4	74.8	1502	2	PCT-US98-23674-2	Sequence 2, Appl
13	1086.4	74.8	1502	37	US-09-894-467-2	Sequence 2, Appl
14	1044.6	71.9	1490	38	US-09-900-876-2	Sequence 2, Appl
15	1044.6	71.9	60918	44	US-10-015-127-578	Sequence 578, App
16	1035.6	71.3	1446	7	US-08-249-901-4	Sequence 4, Appl
17	1026	70.7	1446	7	US-08-249-901-6	Sequence 6, Appl
18	999.6	68.8	1423	7	US-08-249-901-3	Sequence 3, Appl
19	988.6	68.1	1437	7	US-08-249-901-5	Sequence 5, Appl
20	973.6	67.1	1436	38	US-09-902-693-2	Sequence 2, Appl
21	960.4	66.1	1438	38	US-09-902-693-1	Sequence 2, Appl
22	904.8	62.3	1208	1	PCT-US98-23674-1	Sequence 1, Appl
23	904.8	62.3	1208	2	PCT-US98-23674-1	Sequence 1, Appl
24	904.8	62.3	1208	37	US-09-894-467-1	Sequence 1, Appl
25	881.4	60.7	105184	35	US-09-847-513A-1	Sequence 1, Appl
26	870	59.9	1532	1	PCT-US02-41014-38	Sequence 38, Appl
27	870	59.9	1532	44	US-10-029-397A-38	Sequence 38, Appl
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29	869.8	59.9	1532	44	US-10-007-725-6	Sequence 6, Appl
30	869.8	59.9	1532	44	US-10-049-626B-5	Sequence 1, Appl
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32	861.8	59.4	1501	33	US-09-791-592-1	Sequence 1, Appl
33	861.8	59.4	1501	33	US-09-791-610-1	Sequence 1, Appl
34	861.8	59.4	1501	41	US-09-951-720-1	Sequence 1, Appl
35	861.8	59.4	1501	46	US-10-103-305-1	Sequence 1, Appl
36	861.8	59.4	1501	46	US-10-103-404A-1	Sequence 1, Appl
37	861.8	59.4	1501	48	US-10-218-519-5	Sequence 5, Appl
38	861.8	59.4	1501	48	US-10-242-696-1	Sequence 1, Appl
39	861.8	59.4	1501	49	US-10-252-518-5	Sequence 5, Appl
40	861.8	59.4	1501	49	US-10-266-787-5	Sequence 5, Appl
41	861.8	59.4	1501	52	US-10-411-319-1	Sequence 1, Appl
42	861.6	59.3	25132	62	US-60-082-302-750	Sequence 750, App
43	857.6	59.1	1540	49	US-10-360-647-1	Sequence 1, Appl
44	854.6	58.9	1535	1	PCT-US02-41014-41	Sequence 41, Appl
45	854.6	58.9	1535	14	US-08-923-030-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-856-640-1

Sequence 1, Application US/09856640

GENERAL INFORMATION:

APPLICANT: TSUBOKURA, Akira

APPLICANT: IONEDA, Haruyoshi

APPLICANT: MIYATA, Haruyoshi

TITLE OF INVENTION: A PIGMENT-CONTAINING SUBSTANCE FOR FEED ADDITIVES

FILE REFERENCE: 38331-0002

CURRENT APPLICATION NUMBER: US/09/856.640

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: PCT/JP00/06528

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: 279337/1999

PRIOR FILING DATE: 1999-09-30

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 1452

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: DNA nucleotide sequence corresponding to 16S ribosomal RNA

NAME/KEY: variation

LOCATION: (1350)..(1350)

OTHER INFORMATION: n is A or G or C or T

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1261 ATCCGCGAAGACAGCATCCCGGCTGAATACGTTCCCGGGCTTGTACACACCCCGGCTCAC 1320
1261 ATCCGCGAAGACAGCATCCCGGCTGAATACGTTCCCGGGCTTGTACACACCCCGGCTCAC 1320
1321 ACATGGGAGTGGTCTACCGAGACAGTGGCTTAACCTTCGGGGGCGACGGCGCCAC 1380
1321 ACCATGGGAGTGGTCTACCGAGACAGTGGCTTAACCTTCGGGGGCGACGGCGCCAC 1380
1381 GGTAGATCAGGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTTCGGGCTG 1440
1381 GGTAGATCAGGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTTCGGGCTG 1440
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RESULT 3

US-10-049-228-2
; Sequence 2, Application US/10049228
; GENERAL INFORMATION:
; APPLICANT: TSUBOKURA, Akira
; TITLE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS
; FILE REFERENCE: 38331-0003
; CURRENT APPLICATION NUMBER: US/10/049,228
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/04874
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: JP 2000-175124
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA of A-5
; OTHER INFORMATION: 81-1 strain
US-10-049-228-2

Query Match 95.0%; Score 1380; DB 44; Length 1426;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
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4 AGTTTGATCTGCTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGA 63
61 GACCTTCGGGCTAGCGGGGACGGGTGAGTAACGCTGGGACGTCCTCTCTACGG 120
64 GACCTTCGGGCTAGCGGGGACGGGTGAGTAACGCTGGGACGTCCTCTCTACGG 123
121 AATAGCCCGGGAACATGGGAGTAATACCGTATACGCCCTTTGGGGGAAGATTATTCGG 180
124 AATAGCCCGGGAACATGGGAGTAATACCGTATACGCCCTTTGGGGGAAGATTATTCGG 183
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244 ATCCATAGCTGGTTTACAGAGGATGATCAGCCACATCGGGACTCAGACACCGCCAGACTC 303
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361 GGGTGAAGTCAAGAGCCCTTAGGGTTGTAAGCTCTTTTTCAGCTGGGAAATATGACGCT 420
364 GGGTGAAGTCAAGAGCCCTTAGGGTTGTAAGCTCTTTTTCAGCTGGGAAATATGACGCT 423
421 ACCAGCAGAAAGAGCCCGGCTTAACCTCCGTCAGCAGCAGCGGGTAAATACGAGGGGGCT 480
424 ACCAGCAGAAAGAGCCCGGCTTAACCTCCGTCAGCAGCAGCGGGTAAATACGAGGGGGCT 483
481 AGCGTTGTTTCGGAATTAACCTGGGGTAAAGCGCAGCTAGGCGGACTGGAAGTCAAGAGTG 540
484 AGCGTTGTTTCGGAATTAACCTGGGGTAAAGCGCAGCTAGGCGGACTGGAAGTCAAGAGTG 543
541 AATCCCGGCTCAACCTTGGAACTGCGCTTGAAGTCAAGTATTCAGTCTGGAGTTGAGAGAG 600
544 AATCCCGGCTCAACCTTGGAACTGCGCTTGAAGTCAAGTATTCAGTCTGGAGTTGAGAGAG 603
601 GTGAGTGAATTCGAGAGTGAAGTTCGTAAGTTCGTAAGTTCGTAAGTTCGTAAGTTCGTAAG 660
604 GTGAGTGAATTCGAGAGTGAAGTTCGTAAGTTCGTAAGTTCGTAAGTTCGTAAGTTCGTAAG 663
661 GAAGCGGCTCACTGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 720
664 GAAGCGGCTCACTGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 723
721 ATTAGATACCTGGTGTAGTCCACCCGCTTAACGATGAATGCGGAGTTCGCGGAGCATGCT 780
724 ATTAGATACCTGGTGTAGTCCACCCGCTTAACGATGAATGCGGAGTTCGCGGAGCATGCT 783
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784 TGTGCTGTGTCACACCTTAACGATGAATGCGGAGTTCGCGGAGTTCGCGGAGCATGCT 843
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844 AACTCAAAGGAATTAACGAGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 903
901 AAGCGCGAGAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCTTACCAAC 960
904 AAGCGCGAGAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCTTACCAAC 963
961 CGTAAGAGACCTCGACACAGGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1020
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RESULT 4

US-10-166-225A-12
; Sequence 12, Application US/10166225A
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/10/166,225A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Paracoccus sp. R-1512
US-10-166-225A-12

Query Match 88.5%; Score 1285.2; DB 47; Length 1404;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 59; Indels 3; Gaps 2;

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QY	90	GTAACGCTGGGAAAGCTGCTCTACGGAATAGCCCCGGGAACTGGGAGTAATACC	149
DB	61	GTAACGCTGGGAAAGCTGCTCTACGGAATAGCCCCGGGAACTGGGTTTAAATACC	120
QY	150	GTAACGCTGGGAAAGCTTATCGGAGAGGATCGGCGCGCTGGATAGGTA	209
DB	121	GTAACGCTGGGAAAGCTTATCGGAGAGGATCGGCGCGCTGGATAGGTA	180
QY	210	GTTGGTGGGTAATGGCCCAAGCCAGCATCATAGCTGGTGTGAGAGATGATCAG	269
DB	181	GTTGGTGGGTAATGGCCCAAGCCAGCATCATAGCTGGTGTGAGAGATGATCAG	240
QY	270	CCACACTGGGACTGAGACACCGCCAGACTCCTACGGGAGGAGCAGTGGGAACTTAG	329
DB	241	CCACACTGGGACTGAGACACCGCCAGACTCCTACGGGAGGAGCAGTGGGAACTTAG	300
QY	330	ACAATGGGGCAACCTGATCTAGCCATCGCGCTGAGTGATGAAGGCTTAGGTTGTA	389
DB	301	ACAATGGGGCAACCTGATCTAGCCATCGCGCTGAGTGATGAAGGCTTAGGTTGTA	360
QY	390	AAGCTCTTACGCTGGGAAAGATATGACGGTACACGAGAGAGAGAGCCCGGCTAACTCCG	449
DB	361	AAGCTCTTACGCTGGGAAAGATATGACGGTACACGAGAGAGAGAGCCCGGCTAACTCCG	420
QY	450	TGCCAGACGCGCGTAAATCGGAGGCGCTAGCGTCTCGGAATTAATCGGCTAAAG	509
DB	421	TGCCAGACGCGCGTAAATCGGAGGCGCTAGCGTCTCGGAATTAATCGGCTAAAG	480
QY	510	CGCAGTGGGAGTGGAAAGTACAGAGTGAATCCCGGGCTCAACCTTGGAACTGCC	569
DB	481	CGCAGTGGGAGTGGAAAGTACAGAGTGAATCCCGGGCTCAACCTTGGAACTGCC	540
QY	570	TTTGAAATATCATGCTCGAGTTCGAGAGAGTGAATTCGAGTGTAGAGGTGAA	629
DB	541	TCCAAAATCATCATGCTCGAGTTCGAGAGAGTGAATTCGAGTGTAGAGGTGAA	600
QY	630	ATTGCTAGATATTCGAGAGACACACAGTGGGAGGCGGCTCACTGGCTCGATACGACG	689
DB	601	ATTGCTAGATATTCGAGAGACACACAGTGGGAGGCGGCTCACTGGCTCGATACGACG	660
QY	690	CTGAGGTCGGAAGCGTGGGAGCAACAGGATAGATACCTGCTAGTCCACGCGGTAA	749
DB	661	CTGAGGTCGGAAGCGTGGGAGCAACAGGATAGATACCTGCTAGTCCACGCGGTAA	720

QY	750	ACGATGAATGCCAGACGTCGGCAAGCATGCTTGTGGTGTACACCTAACGATTAAGCA	809
DB	721	ACGATGAATGCCAGTCGTCGGGTGCAATTCGGTGACACCTAACGATTAAGCA	780
QY	810	TTCGCCCTGGGAGTACGTCGCAAGATTAATACTCAAGGAATTAAGCGGGGCGCGCAC	869
DB	781	TTCGCCCTGGGAGTACGTCGCAAGATTAATACTCAAGGAATTAAGCGGGGCGCGCAC	840
QY	870	AAGCGGTGAGCATGTGGTTTAAATTCGAAGCAACGCGCAAGACCTTACCAACCTTGACA	929
DB	841	AAGCGGTGAGCATGTGGTTTAAATTCGAAGCAACGCGCAAGACCTTACCAACCTTGACA	900
QY	930	TGGCAGGACCGCTGGAGAGATTCAGCTTCTCGTAAGAGACCTGCACACAGTGTGCTAT	989
DB	901	TCCCTGGACATCCCGAGAGATCGGCTTTTAACTTCGGTGACGAGAGAGTGTGCTAT	960
QY	990	GGCTGTGTCAGCTCGTGTGAGATGTCGGTTAAGTCCGCAACGAGCGCAACCCAC	1049
DB	961	GGCTGTGTCAGCTCGTGTGAGATGTCGGTTAAGTCCGCAACGAGCGCAACCCAC	1020
QY	1050	GTCCCTAGTGGCAGCAATTCAGTTGGGAACCTCTATGGAACCTGCCGATGATGATCGGA	1109
DB	1021	GTCCCTAGTGGCAGC-ATTCAATTGGGCACTCTATGGAACCTGCCGATGATGATCGGA	1079
QY	1110	GGAAGGTGGATGACGTCAGTCTCATGCGGCTTACGGTTGGGCTACACACGTCGTA	1169
DB	1080	GGAAGGTGGATGACGTCAGTCTCATGCGGCTTACGGTTGGGCTACACACGTCGTA	1139
QY	1170	CAATGCTGTGACAGTGGGTTAATCCCAAGAGCCTATCAGTTCGGATGCTCTGCA	1229
DB	1140	CAATGCTGTGACAGTGGGTTAATCCCAAGAGCCTATCAGTTCGGATGCTCTGCA	1199
QY	1230	ACTCAGGAGCATGAAGTTGGAATCGCTAGTAATCGCGAAGCAGCATGCCGCTGAATAC	1289
DB	1200	ACTCAGGAGCATGAAGTTGGAATCGCTAGTAATCGCGAAGCAGCATGCCGCTGAATAC	1259
QY	1290	GTTCGCCGCGCTGTGACACACCGCGCTCACACCATGGAGTGGTTCCTACCGGACGAG	1349
DB	1260	GTTCGCCGCGCTGTGACACACCGCGCTCACACCATGGAGTGGTTCCTACCGGACGAG	1319
QY	1350	NTGCCCTAAC-TCGCGGGGACGCGGCGCAGGTAGGATCAGGCTGGGTTGAAGTC	1407
DB	1320	CTGCCCTAACCTTCGGGAGGAGCGGCGCAGGTAGGATCAGGCTGGGTTGAAGTC	1379
QY	1408	GTAACAAGGTAGCCGTAGGGGAACC	1432
DB	1380	GTAACAAGGTAGCCGTAGGGGAACC	1404

RESULT 5

US-60-296-299-12
; Sequence 12, Application US/60296299
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne
; APPLICANT: YELISEEV, Alexei
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/60/296,299
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Paracoccus sp. R-1512
US-60-296-299-12

Query Match

88.5%; Score 1285.2; DB 84; Length 1404;

1021	GTCCCTAGTTGCCAGC - ATTCACTTGGCGACTCTATGGAACACTGCCGATGATAAGTCGGA	1079
Db		
1110	GGAAGTGTGGATGACGCTCAAGTCCCTCATGGGCCCTTACGGTTGGCTACACACGTCGCTA	1169
Qy		
1080	GGAAGTGTGGATGACGCTCAAGTCCCTCATGGGCCCTTACGGTTGGCTACACACGTCGCTA	1139
Db		
1170	CAATGGTGGTGACAGTGGGTTAATCCGCAAAAGCCATCTCAGTTCGGATGTCTCTGCA	1229
Qy		
1140	CAATGGTGGTGACAGTGGGTTAATCCGCAAAAGCCATCTCAGTTCGGATGTCTCTGCA	1199
Db		
1230	ACTCGAGGGCATCAAGTTGGAATCGCTAGTAATCGCGGAACACGATGCCGGTGAATAC	1289
Qy		
1200	ACTCGAGGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACACGATGCCGGTGAATAC	1259
Db		
1290	GTTCCCGGGCCTTGATACACACCCCGCGTCACACCATGGGAGTTGGTTCTACCCGACGACG	1349
Qy		
1260	GTTCCCGGGCCTTGATACACACCCCGCGTCACACCATGGGAGTTGGTTCTACCCGACGACG	1319
Db		
1350	NTGCGCTAAC - TTCCGGGGGCGAGCGGCCACGGTAGGATACAGCGACTGGGGTGAAGTC	1407
Qy		
1320	CTGCGTCACTCCCTTCGGGGAGGCGAGCGGCCACGGTAGGATCAGCGACTGGGGTGAAGTC	1379
Db		
1408	GTAACAAGGTAGCCGTAGGGGAACC	1432
Qy		
1380	GTRACAAGGTAGCCGTAGGGGAACC	1404
Db		

	Query Match	83.5%;	Score 1212.6;	DB 32;	Length 1385;
	Best Local Similarity	93.6%;	Pred. No. 0;		
	Matches 1297;	Conservative 0;	Mismatches 85;	Indels 4;	Gaps 3;
Qy	18	GAACGACGGTGGCGGCAGCCTTAACACATGTCAGTGACGGAGACCTTCGGGTCTAGCG	77		
Db	1385	GAACGAAACGTTGGCGCAGGCCCTAACACATGCAAGTCGACGAGAGACTTCGGTCCCTAGCG	1326		
Qy	78	GCGGACGGGTGAGTAACGCGTGGGAACGTTGCCCTTCTCTACGGAATAAGCCCCGGGAAACT	137		
Db	1325	GCGGACGGGTGAGTAACGCGTGGGAACGTTGCCCTTCTCGGNATAGCCCTGGGAAACT	1266		
Qy	138	GGGAGTAATACCCTPATACGC-CCTTTGGGGGAAGAATTATTCGGAGAAGGATCGGCCCGC	196		
Db	1265	GGGAGTAATACCGGATACGCTCTTTTTGAGGAAGATTATTCGGCGAAGGATCGGCCCGC	1206		
Qy	197	GTTGGATAGGTAGTTGTTGGGTAAATGGCCCACCAAGCCGACGATCCATAGCTGTTGTTG	256		
Db	1205	GTTGGATTAGTGTGTTGGGTAAATGTCCTACCAAGCCGACGATCCATAGCTGTTGTTG	1146		
Qy	257	AGAGGATGATCAGCCCACTGGGACTGAGACACGGGCCCACTCTTACGGGAGGCACGAG	316		
Db	1145	AGAGGATGATCAGCCCACTGGGACTGAGACACGGGCCCACTCTTACGGGAGGCACGAG	1086		

QY 317 TGGGAATCTTAGCAATGGGGCAACCCCTGATCTAGCCATGCCGCTGAGTGATGAAGG 376
DB |||||||
QY 1085 TGGGAATCTTAGCAATGGGGCAACCCCTGATCTAGCCATGCCGCTGAGTGATGAAGG 1026
DB |||||||
QY 377 CCTTAGGGTTCTAAAGCTCTTTACGCTGGGAGATAATGACGGTACCAGAGAAAGCC 436
DB |||||||
QY 1025 CCTTAGGGTTCTAAAGCTCTTTACGCTGGGAGATAATGACGGTACCAGAGAAAGCC 966
DB |||||||
QY 437 CCGCTACTCCGTCAGCAGCCGCGTATACGGAGGGGCTAGCGTTGTCGGAATT 496
DB |||||||
QY 965 CCGCTACTCCGTCAGCAGCCGCGTATACGGAGGGGCTAGCGTTGTCGGAATT 906
DB |||||||
QY 497 ACTGGGCTAAAGCGCAGTGGGCGACTGGAAGTCAAGAGTGAATCCAGGGCTCAA 556
DB |||||||
QY 905 ACTGGGCTAAAGCGCAGTGGGCGACTGGAAGTGGGGTGAATCCCGGGCTCAA 846
DB |||||||
QY 557 CTTTGGAACTCCCTTTGAACTATCAGTCTGGAGTTCGAGAGAGTGAATTCGGA 616
DB |||||||
QY 845 CCGGGAATCGCTTCAAACCTGTCAGTCTGGAGTTCGAGAGAGTGAATTCGGA 786
DB |||||||
QY 617 GTGTAGAGTGAATTCGATATATTCGAGAGACACAGTGGCGAAGCGGCTACTGG 676
DB |||||||
QY 785 GTGTAGAGTGAATTCGATATATTCGAGAGACACAGTGGCGAAGCGGCTACTGG 726
DB |||||||
QY 677 CTCGATCTGAGCTGAGGTGCGAAAGCGTGGGAGCAACAGAGATTAGATACCCTGGA 736
DB |||||||
QY 725 CTCGATCTGAGCTGAGGTGCGAAAGCGTGGGAGCAACAGAGATTAGATACCCTGGA 666
DB |||||||
QY 737 GTCCACGCGTAAACGATGAATGCCAGAGCTCGGCAAGCATGCTTGTGCTGTCACACT 796
DB |||||||
QY 665 GTCCACGCGTAAACGATGAATGCCAGTCTCGGCGACATGCTGTTCCGTTGACACACT 606
DB |||||||
QY 797 AACGGATTAACGATTCGCCCTGGGGAGTACGGTGCAGAGATTAACAACTCAAAGGAATTGA 856
DB |||||||
QY 605 AACGGATTAACGATTCGCCCTGGGGAGTACGGTGCAGAGATTAACAACTCAAAGGAATTGA 546
DB |||||||
QY 857 CGGGGCGCCGACAGCGGTGGAGCATGTGTTTAAATTCGAAGCAACCGCGAGACCTTA 916
DB |||||||
QY 545 CGGGGCGCCGACAGCGGTGGAGCATGTGTTTAAATTCGAAGCAACCGCGAGACCTTA 486
DB |||||||
QY 917 CCAACCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTTCTGTAAGAGACCTGCAC 976
DB |||||||
QY 485 CCAACCTTGACATGGCAGGACCGCACAGAGATGGTGTTCCTCTTCGGGCGCGGAG 426
DB |||||||
QY 977 ACAGGTGCTGATGGCTGCTCAGCTGCTGCTGAGATGTTCGGTTAAGTCCGGCAAC 1036
DB |||||||
QY 425 ACAGGTGCTGATGGCTGCTCAGCTGCTGCTGAGATGTTCGGTTAAGTCCGGCAAC 366
DB |||||||
QY 1037 GAGCGCAACCCACGTCCTTAGTTCGAGCAATTCAGTTGGGAATCTATGGAACCTGCGG 1096
DB |||||||
QY 365 GAGCGCAACCCACACTTCCAGTTGCCATFC - ATTCCGTTGGGCACTCTGGAAGAACTGCGG 307
DB |||||||
QY 1097 ATGATAAGTCGGAGGAGGTGGTGGATGACGTCAAGTCTCATGGGCTTACGGGTTGGCC 1156
DB |||||||
QY 306 ATGATAAGTCGGAGGAGGTGGTGGATGACGTCAAGTCTCATGGGCTTACGGGTTGGCC 247
DB |||||||
QY 1157 TACACAGTGTCTCAATGGTGGTGACAGTGGGTTAATCCCAAGGCAATCTCATGTTGGG 1216
DB |||||||
QY 246 TACACAGTGTCTCAATGGGCTGACAAATGGGTTAATCCCAAGGCAATCTCATGTTGGG 187
DB |||||||
QY 1217 ATTGCTCTCTCAACTCGAGGGCATGAATTTGGATTCGCTAGTATTCGCGGAACAGCATG 1276
DB |||||||
QY 186 ATTGGGCTCTCAACTCGAGCCCATGAATTTGGATTCGCTAGTATTCGCGGAACAGCATG 127
DB |||||||
QY 1277 CCGGGTGAATACACTTCCGGGCTTGTACACACCGCCGCTCACACCATGGAGTTGGTT 1336
DB |||||||
QY 126 CCGGGTGAATACACTTCCGGGCTTGTACACACCGCCGCTCACACCATGGAGTTGGTT 67
DB |||||||
QY 1337 CTACCCGAGCAGNCTGCGCTAACCC - TTTCGGGGGCGAGCGGCGCCACCGGTAGGATCAGCGA 1394
DB |||||||
QY 66 CTACCCGAGCAGNCTGCGCTAACCCCTTACGGGAGCAGCGGACCGGTAGGCTCAGCGA 7

QY 1395 CTGGGG 1400
DB |||||||
DB 6 CTGGGG 1
RESULT 7
US-60-171-140-1/c
; Sequence 1, Application US/60171140
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; TITLE OF INVENTION: Industrial Wastewater BioReactors
; FILE REFERENCE: BC1033 US PV
; CURRENT APPLICATION NUMBER: US/60/171,140
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Paracoccus sp
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain EMB
US-60-171-140-1
Query Match 83.5%; Score 1212.6; DB 71; Length 1385;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 1297; Conservative 0; Mismatches 85; Indels 4; Gaps 3;
QY 18 GAACGAACGCTGGCGGAGGCTTAACACATGCAAGTTCGAGCGAGACCTTCGGGTCTAGCG 77
DB |||||||
QY 1385 GAACGAACGCTGGCGGAGGCTTAACACATGCAAGTTCGAGCGAGACCTTCGGGTCTAGCG 1326
DB |||||||
QY 78 GCGGACGCGGTGAGTAACGCTGGGAAACGCTGCTTCTTACGGAATAGCCCGGGAACCT 137
DB |||||||
QY 1325 GCGGACGCGGTGAGTAACGCTGGGAAACGCTGCTTCTTTCGGAATAGCCCTGGGAACCT 1266
DB |||||||
QY 138 GGGAGTAATACCGTATACGC - CCTTTGGGGGAAAGATTATTCGGAGAGAGATTCGCCCGC 196
DB |||||||
QY 1265 GGGAGTAATACCGTATACGCCTCTTTTGGAGAAAGATTATTCGGCGAAGGATCGGCCCGC 1206
DB |||||||
QY 197 GTTGATTAGTAGTTGTTGGGTAATGCGCCACCAAGCCGACGATCCATAGCTGGTTG 256
DB |||||||
QY 1205 GTTGATTAGTAGTTGTTGGGTAATGCGCTTACCAAGCCGACGATCCATAGCTGGTTG 1146
DB |||||||
QY 257 AGAGGATGATCAGCCACACTGGGACTGAGACACGCCGCCAGACTCTAGCGGAGGCGAGCAG 316
DB |||||||
QY 1145 AGAGGATGATCAGCCACACTGGGACTGAGACACGCCGCCAGACTCTAGCGGAGGCGAGCAG 1086
DB |||||||
QY 317 TGGGAATCTTAGCAATGGGGCAACCCCTGATCTAGCCATGCCGCTGAGTGATGAAGG 376
DB |||||||
QY 1085 TGGGAATCTTAGCAATGGGGCAACCCCTGATCTAGCCATGCCGCTGAGTGATGAAGG 1026
DB |||||||
QY 377 CTTTAGGGTTGTAAGCTCTTTACGCTGGGAGATAATGACGGTACCAGAGAAAGCC 436
DB |||||||
QY 1025 CTTTAGGGTTGTAAGCTCTTTACGCTGGGAGATAATGACGGTACCAGAGAAAGCC 966
DB |||||||
QY 437 CCGGCTAACTCCGTCAGCAGCCGCGTATACGGAGGGGCTAGCGTTGTCGGAATT 496
DB |||||||
QY 965 CCGGCTAACTCCGTCAGCAGCCGCGTATACGGAGGGGCTAGCGTTGTCGGAATT 906
DB |||||||
QY 497 ACTGGGCTAAAGCGCAGTGGGCGACTGGAAGTTCGAGAGTGAATCCAGGGCTCAA 556
DB |||||||
QY 905 ACTGGGCTAAAGCGCAGTGGGCGACTGGAAGTTCGAGAGTGAATCCCGGGCTCAA 846
DB |||||||
QY 557 CTTTGGAACTCCCTTTGAACTATCAGTCTGGAGTTCGAGAGAGTGAATTCGGA 616
DB |||||||
QY 845 CCGGGAATCGCTTCAAACCTGTCAGTCTGGAGTTCGAGAGAGTGAATTCGGA 786
DB |||||||
QY 617 GTGTAGAGTGAATTCGATATATTCGAGAGACACAGTGGCGAAGCGGCTACTGG 676
DB |||||||

785 GTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCACTGGCGAAGCGGCTCACTGG 726
Db
Qy 677 CTCGATACCTACCTGAGTGCCTAAGAGCGTGGGAGCAACACAGATTAGTACCTCGGTA 736
Db
725 CTCGATACCTACCTGAGTGCCTAAGAGCGTGGGAGCAACACAGATTAGTACCTCGGTA 666
Qy 737 GTCCAGCGCCATAACGATGAATGCCAGACGTCGCGCAAGCATGCTTGTGGGTGTACACCT 796
Db
665 GTCCAGCGCCATAACGATGAATGCCAGTCTGTCGCGCAGCATGCTTGTGGGTGACACCT 606
Qy 797 AACGGATTAAAGATTTCGCTCGGAGTACGGTTCGCAAGATTAAACTCAAGAAATTGA 856
Db
605 AACGGATTAAAGATTTCGCTCGGAGTACGGTTCGCAAGATTAAACTCAAGAAATTGA 546
Qy 857 CGGGGGCCGCAAGCGGTGGAGCATGCTGTTTAAATTCGAACACGCGCAGACCTTA 916
Db
545 CGGGGGCCGCAAGCGGTGGAGCATGCTGTTTAAATTCGAACACGCGCAGACCTTA 486
Qy 917 CCACCTTTGACATGGCAGACCGCTGGAGAGATTACAGCTTTCTCGTAAGAGACCTGCAC 976
Db
485 CCACCTTTGACATCTCGACCGCACACAGATGTTTCCCTTTTCGGGCGGGAG 426
Qy 977 ACAGGTCTGATGGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTG 1036
Db
425 ACAGGTCTGATGGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTG 366
Qy 1037 GAGCGCAACCCAGTCCCTAGTTGCCAGCAATTCAGTTGGGAATCTATGGAACCTGCCG 1096
Db
365 GAGCGCAACCCAGTCCCTAGTTGCCATC-ATTCGGTTGGGCACCTTGGGAACCTGCCG 307
Qy 1097 ATGATAGTGGGAGAGGTGTGGATGACGCTCAAGTCTCATGGGCTTACGGGTTGGGC 1156
Db
306 ATGATAGTGGGAGAGGTGTGGATGACGCTCAAGTCTCATGGGCTTACGGGTTGGGC 247
Qy 1157 TACACAGTGTCAATGGTGGTGACAGTGGGTTAATCCCAAAAGCCATCTCAGTTCGG 1216
Db
246 TACACAGTGTCAATGGTGGTGACAGTGGGTTAATCCCAAAAGCCGCTCAGTTCGG 187
Qy 1217 ATTGTCTCTGCACTCGAGGATGATGATGATGATGATGATGATGATGATGATGATG 1276
Db
186 ATTGGGTCTGCACTCGAGCCCTGATGATGATGATGATGATGATGATGATGATGATG 127
Qy 1277 CCGGGTGAATACCTTCCGGGCTTGTACACACCGCCGCTCACACCATGGAGTTGGTT 1336
Db
126 CCGGGTGAATACCTTCCGGGCTTGTACACACCGCCGCTCACACCATGGAGTTGGTT 67
Qy 1337 CTACCCGACGAGTGGCTTAACC--TTCGGGGGCGAGCGGCGCCACGATGATGATG 1394
Db
66 CTACCCGACGCGCTGGCTAACCTTACGGGAGGACGCGACCGTAGGCTACGCGA 7
Qy 1395 CTGGGG 1400
Db 6 CTGGGG 1

RESULT 8

US-09-739-449-191

; Sequence 191, Application US/09739449

; GENERAL INFORMATION:

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(13490)C

; CURRENT APPLICATION NUMBER: US/09739,449

; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: US 09/514,000

; PRIOR FILING DATE: 2000-02-23

; NUMBER OF SEQ ID NOS: 13351

; SEQ ID NO 191

; LENGTH: 20310

; TYPE: DNA

; ORGANISM: Agrobacterium tumefaciens

US-09-739-449-191

Query Match 76.7%; Score 1113; DB 32; Length 20310;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 1288; Conservative 0; Mismatches 161; Indels. 29; Gaps 5;
Qy 1 AGTTTATCTCTGCTCAGAACGCTGCGGAGGCTTAAACACATGCAAGTGCAGCGA 60
Db 17520 AGTTTATCTCTGCTCAGAACGCTGCGGAGGCTTAAACACATGCAAGTGCAGAAC-- 17577
Qy 61 GACCTTCGGTCTAGCGGCGGAGGCTGAGTAACCGCTGAGGAGCGCTTCTCTACGG 120
Db 17578 GCGCCGCAAGGGAGTGGAGAGCGGTGAGTAACCGCTGAGGAGTCTACCATCTCTCGG 17637
Qy 121 AATAGCCCGGGAACCTGGGAGTAATACCGCTATACGCCCTTTGGGGGAAAGATTATTCGG 180
Db 17638 AATAGCTCTGGGAACCTGGGAGTAATACCGCTATACGCCCTTACGGGGAAAGATTATTCGG 17697
Qy 181 ASAAGATCGCCCGCTTGGATTAGTGTGGGTAAATGGCCACCAAGCCGACG 240
Db 17698 GGATGGATGAGCGCGCTTGGATTAGTGTGGGTAAAGGCCCTACCAAGCGCAGC 17757
Qy 241 ATCATAGCTGTTTGGAGAGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC 300
Db 17758 ATCATAGCTGTTTGGAGAGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC 17817
Qy 301 CTACGGGAGGACGAGTGGGGAATCTTACCAATGGGGGCAACCTCTGATCAGCCATGCC 360
Db 17818 CTACGGGAGGACGAGTGGGGAATCTTGGCAATGGGGGCAACCTCTGATCAGCCATGCC 17877
Qy 361 GCCTGATGATGAAGCGCTTAGGGTTGTAAAGCTCTTTTACGCTGGGAGAGTAATGACGGT 420
Db 17878 GCCTGATGATGAAGCGCTTAGGGTTGTAAAGCTCTTTTACGCTGGGAGTAATGACGGT 17937
Qy 421 ACCAGCAGAAAGACCCCGGCTAACTCGTGCAGACGCGCGGTATACGGAGGGGGCT 480
Db 17938 AGTCGGAAGAAGACCCCGGCTAACTCGTGCAGACGCGCGGTATACGGAGGGGGCT 17997
Qy 481 AGCGTGTCTCGGAATTAAGCGCTAAAGCGCAGTGGGCGACTGGAAGTCAAGAGTG 540
Db 17998 AGCGTGTCTCGGAATTAAGCGCTAAAGCGCAGTGGGCGACTGGAAGTCAAGAGTG 18057
Qy 541 AAATCCAGCGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTCTGAGAGAGAG 600
Db 18058 AAATCCAGCGCTCAACCTGCGAACTGCTTTGATCTGGGTATCTTGGATGGAAGAG 18117
Qy 601 GTGAGTGAATTCGAGTGTAGAGGTGAATTCCTAGATATTCGGAGAACACACAGTGGC 660
Db 18118 GTAGTGAATTCGAGTGTAGAGGTGAATTCCTAGATATTCGGAGAACACACAGTGGC 18177
Qy 661 GAAGCGGCTCACTGGCTCGATCTGAGCTGAGTGGCGAAGCGTGGGAGCAACAGG 720
Db 18178 GAAGCGGCTCACTGGCTCGATCTGAGCTGAGTGGCGAAGCGTGGGAGCAACAGG 18237
Qy 721 ATTAGATACCTTGTGTAGTCCAGCGCTAAACAGATGAATGCCAGACGCTCGGCAAGCATGCT 780
Db 18238 ATTAGATACCTTGTGTAGTCCAGCGCTAAACAGATGAATGTAGCGCTCGGCAAGTACT 18297
Qy 781 TGTGCTGTACACCTTAACGATTAAGCATTTCCGCTGGGGAGTACGGTGCACAGATTAA 840
Db 18298 GTTCGGTGGCGAGCTAACGCATTAACATTTCCGCTGGGGAGTACGGTGCACAGATTAA 18357
Qy 841 AACTCAAGGAATTAAGCGGGGCGCCGACAGCGGTGAGCATCTGGTTTAAATTCGAGC 900
Db 18358 AACTCAAGGAATTAAGCGGGGCGCCGACAGCGGTGAGCATCTGGTTTAAATTCGAGC 18417
Qy 901 AACGCGCAGAACCTTACCAACCTTGACAT----GGCAGGACCGCTGGAGAGATTACGCT 956
Db 18418 AACGCGCAGAACCTTACCAACCTTGACATTCGCGGTATGGGCATTTGGAGACGATGCTCT 18477
Qy 957 TTCTCGTAAGAGACCTGCACACAGGCTGCTGCATGGCTGTCTGCTACGCTGCTGCTGAGAT 1016
Db 18478 TCAGTTAGGCTGGCCCCCAGAACAGGTGCTGCATGGCTGTCTGCTACGCTGCTGCTGAGAT 18537

QY 1017 GTTCGGTTAAGTCCGGCAAGGAGCGCAACCCACGTCCTCCTAGTTCCAGCAATTCAGTTGG 1076
DB 18538 GTTCGGTTAAGTCCGGCAAGGAGCGCAACCCACGTCCTCCTAGTTCCAGCAATTCAGTTGG 18596
QY 1077 GAACCTCATGGAACACTCCGATGATAGTCG-GAGGAAGGTGTGGATGACGTCAAGTCCT 1135
DB 18597 GCACCTCAAGGGGACTCCGCTGATAGAGCGAGAGGAGGTGGGATGACGTCAAGTCCT 18656
QY 1136 CATGGGCTTACGGGTTGGGCTACACACGTCGTACAAATGTTGTTGACAGTGG----- 1187
DB 18657 CATGGGCTTACGGGTTGGGCTACACACGTCGTACAAATGTTGTTGACAGTGG----- 1187
QY 1188 -----GTTAATCCCAAGGCACTCAGTTCGGATTGCTCCTGCAACTCG 1234
DB 18717 ACAGCGATGTCGAGCTAATCTCCAAAGGCACTCAGTTCGGATTGCTCCTGCAACTCG 18776
QY 1235 AGGCATGAAGTTGGATCGTAGTAAATCGGGAACAGATCGCGGGTGAATACGTTCC 1294
DB 18777 AGTCATGAAGTTGGATCGTAGTAAATCGGGAACAGATCGCGGGTGAATACGTTCC 18836
QY 1295 CGGSCCTTGACACACGCGCGTCACACCATGGGAGTTGGTCTACCGGACGAGCGTCCG 1354
DB 18837 CGGSCCTTGACACACGCGCGTCACACCATGGGAGTTGGTCTACCGGACGAGCGTCCG 18896
QY 1355 CTAACCTTCGGGGGAGCGCGCCACCGTAGGATCAGCGACTGGGGTGAAGTCTGAACAA 1414
DB 18897 CTAACCGCAAGGAGCGAGCTAACCCAGGTAGGTCAGCGACTGGGGTGAAGTCTGAACAA 18956
QY 1415 GGTAGCGTAGGGGAACCTCGCGCTGGATCAGCTCCCT 1452
DB 18957 GGTAGCGTAGGGGAACCTCGCGCTGGATCAGCTCCCT 18994

RESULT 9

US-09-803-110-191
; Sequence 191, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 191
; LENGTH: 20310
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-191

Query Match 76.7%; Score 1113; DB 34; Length 20310;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 1286; Conservative 0; Mismatches 161; Indels 29; Gaps 5;
QY 1 AGTTTGATCTCGGCTCAGAACGAGCGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
DB 17520 AGTTTGATCTCGGCTCAGAACGAGCGCTGGCGGAGGCTTAACACATGCAAGTCGAG-- 17577
QY 61 GACCTTCGGGTCTAGCGCGGAGCGGTGAGTAACCGGTGGGAACGTCGCTCTACGG 120
DB 17578 GCCCGGAAGGGGAGTGCACAGCGGTGAGTAACCGGTGGGAACGTCGCTCTACGG 17637
QY 121 AATAGCCCCGGAACCTGGGAGTAATACCGTATACGCTTGGGGGAAGATTATCGG 180
DB 17638 AATAGCTTGGGAACCTGGGAATTAATACCGTATACGCTTGGGGGAAGATTATCGG 17697
QY 181 AGAAGGATCGCCCGCTTGGATTAGGTAGTTGGTGGGTAATGSCCCCAACGAGCGAG 240

DB 17698 GGATGGATGAGCCCGCTTGGATTAGCTAGTTGGTGGGTAAGAGCCCTACCAAGCGGAGC 17757
QY 241 ATCCATAGCTGGTTGGAGAGGATGATCAGCCACACTGGGACTGAGACAGCGCCAGACTC 300
DB 17758 ATCCATAGCTGGTTGGAGAGGATGATCAGCCACACTGGGACTGAGACAGCGCCAGACTC 17817
QY 301 CTACGGGAGGAGCAGTGGGGAATCTTAGACAATGGGGGCAACCTGATCTAGCCATGCC 360
DB 17818 CTACGGGAGGAGCAGTGGGGAATCTTAGACAATGGGGGCAACCTGATCTAGCCATGCC 17877
QY 361 GCCTGACTGATGAAGGCTTAGGGTTGTAAGCTCTTTTACGCTGGGAAGATAATACCGGT 420
DB 17878 GCCTGACTGATGAAGGCTTAGGGTTGTAAGCTCTTTTACGCTGGGAAGATAATACCGGT 17937
QY 421 ACCAGCAGAAGAACCCCGGCTAACTCCGTGCCAGCACCCCGGTTAATACGAGGGGGCT 480
DB 17938 AGTCGGAGAAGAACCCCGGCTAACTCCGTGCCAGCACCCCGGTTAATACGAGGGGGCT 17997
QY 481 AGCGTTGTTCCGGAATTAAGTGGCGTAAAGCGCACGTAGCGGACTTGGAAAGTCAGAGGTG 540
DB 17998 AGCGTTGTTCCGGAATTAAGTGGCGTAAAGCGCACGTAGCGGACTTGGAAAGTCAGAGGTG 18057
QY 541 AAATCCCAAGGCTCAACCTTGGAACTGCTTTGAAACTATCAGTCTGGAGTTCGAGAGAG 600
DB 18058 AAATCCCAAGGCTCAACCTTGGAACTGCTTTGAAACTATCAGTCTGGAGTTCGAGAGAG 18117
QY 601 GTGAGTGGAAATTCGAGGTGAGAGGTGAAATTCGTAGATATTCGGAGAAACACCACTGGC 660
DB 18118 GTGAGTGGAAATTCGAGGTGAGAGGTGAAATTCGTAGATATTCGGAGAAACACCACTGGC 18177
QY 661 GAAGCGGCTCAGCTGGCTGATACCTGAGCGTGGAGTGGAGGAGGAGGAGCAACAGG 720
DB 18178 GAAGCGGCTCAGCTGGCTGATACCTGAGCGTGGAGTGGAGGAGGAGGAGCAACAGG 18237
QY 721 ATTAGATACCTGGTGTAGTCCAGCGCTAAACGATGAATTCGAGAGCTCGGCAAGCATGCT 780
DB 18238 ATTAGATACCTGGTGTAGTCCAGCGCTAAACGATGAATTCGAGAGCTCGGCAAGCATGCT 18297
QY 781 TGTGGGTCTACACCTAAGGATTAAGCATTTCCGCTGGGAGTACGCTCGCAAGATTAA 840
DB 18298 GTTCGGTGGCGAGCTAAGCATTTAAACATTTCCGCTGGGAGTACGCTCGCAAGATTAA 18357
QY 841 AACTCAAGGAATTAAGCGGGGCGCGCACAGCGGTGAGCATGTGTTTAAATTCGAAGC 900
DB 18358 AACTCAAGGAATTAAGCGGGGCGCGCACAGCGGTGAGCATGTGTTTAAATTCGAAGC 18417
QY 901 AACGCGCAGAACTTACCAACCTTTGACAT----GGCAGGACCGCTGGAGAGATTCACT 956
DB 18418 AACGCGCAGAACTTACCAACCTTTGACATTTGGGCTATGGCAATTTGGAGAGATGCTCT 18477
QY 957 TTCTCGTGAAGACCTGCACAGAGTGTGATGGCTGTCTGTCAGCTCGTCTCGTGAGAT 1016
DB 18478 TCAGTTAGGCTGGCCCGCAGAGAGTGTGATGGCTGTCTGTCAGCTCGTCTCGTGAGAT 18537
QY 1017 GTTCGGTTAAGTCCGGCAACGAGCGCAACCCAGCTCCCTAGTTGGCAGCAATTCAGTTGG 1076
DB 18538 GTTCGGTTAAGTCCGGCAACGAGCGCAACCCAGCTCCCTAGTTGGCAGC-ATTAGTTGG 18596
QY 1077 GAACCTCTAGGAACCTGCCGATGATGAAGTCG-GAGGAAGGTGTGGATGACGTCAAGTCT 1135
DB 18597 GCACCTCTAAGGGAGTCCGCTGATGAAGCGGAGAGGAGGAGGAGTGGGATGACGTCAAGTCT 18656
QY 1136 CATGGGCTTACGGGTTGGGCTACACAGTGTCTACAATGGTGGTGCAGAGTGG----- 1187
DB 18657 CATGGGCTTACGGGTTGGGCTACACAGTGTCTACAATGGTGGTGCAGAGTGG----- 1187
QY 1188 -----GTTAATCCCAAGGCACTCAGTTCGGATTGCTCCTCGCAACTCG 1234
DB 18717 ACAGCGATGTCGAGCTAATCTCCAAAGGCACTCAGTTCGGATTGCTCCTCGCAACTCG 18776
QY 1235 AGGCGATGAAGTTGGAATCGGTAGTAAATCGGGAACAGCATGCGCGGTGAATACGTTCC 1294

RESULT 11
PCT-US98-

Query Match

Best Local Similarity 86.2%; Pred. No. 0; Mismatches 177; Indels 23; Gaps 3;
Matches 1245; Conservative 0;

QY 20 ACAGACGCTGCGGCGGCTTAAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCGG 79
DB 1502 ACAGACGCTGCGGCGGCTTAAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCGG 1443
QY 80 GGAGGGGTAGTAACGCGTGGGAACGTCCTTCTTACGGAATAGCCCCGGGAAATCGG 139
DB 1442 GGAGGGGTAGTAACGCGTGGGAACGTCCTTCTTACGGAATAGCCCCGGGAAATCGG 1383
QY 140 GAGTAATACCTATACGCGCTTGGGGAAGAGATTATCGAGAGAGATCGCCCGGCTT 199
DB 1382 GGCTAATACCGGATACGCGCTTATGGGGAAGAGATTATCGCCGGAAGATCGCCCGGCTC 1323
QY 200 GGATTAGTAGTGTGGTGGGTAATGGCCCAACGACGACGATCCATAGCTGGTTGAGA 259
DB 1322 TGATTAGCTAGTGTGGTGGGTAATGGCCCAACGACGACGATCCATAGCTGGTTGAGA 1263
QY 260 GGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGGACGAGTGG 319
DB 1262 GGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGGACGAGTGG 1203
QY 320 GGAATCTTAGACAATGGGCGCAACCTGATCTAGCCATGCGCGTGAAGTGAAGGCTT 379
DB 1202 GGAATCTTAGACAATGGGCGCAACCTGATCTAGCCATGCGCGTGAAGTGAAGGCTT 1143
QY 380 TAGGTTGTTAAAGCTCTTTCAGCTGGGAAGATATGACGGTACAGCAGAGAAGACCCCG 439
DB 1142 TAGGTTGTTAAAGCTCTTTCAGCTGGGAAGATATGACGGTACAGCAGAGAAGACCCCG 1083
QY 440 GCTAACTCCGTCAGCAGCCGCGTAATACGGAGGGGCTAGCGTTTTCGGAAATTAAT 499
DB 1082 GCTAACTCCGTCAGCAGCCGCGTAATACGGAGGGGCTAGCGTTTTCGGAAATTAAT 1023
QY 500 GGGCTAAAGCGCAGCTAGGCGGACTGGAAGTACAGAGTGAATCCAGGCGCTCAACT 559
DB 1022 GGGCTAAAGCGCAGCTAGGCGGACTGGAAGTACAGAGTGAATCCAGGCGCTCAACT 963
QY 560 TGGAACTCCCTTTGAACTATCAGTCTGAGTTCGAGAGAGTGAAGTGAATTCGAGTGC 619
DB 962 CAGATGCGCTTCGATACCTGGGACGCTGAGTATGATGAGAGTGGTGAAGTGGAGTGC 903
QY 620 TAGAGTGAATTCGTAGATATTCGAGAGACACAGTGGCGAAGGCGGCTCACTGGCTC 679
DB 902 TAGAGTGAATTCGTAGATATTCGAGAGACACAGTGGCGAAGGCGGCTCACTGGCTC 843
QY 680 GATAGTACGCTGAGTGGGAGGCGGAGGAGCAACAGATTAATACCTGGTATGC 739
DB 842 ATTACTGACGCTGAGGCGGAGGCGGAGGAGCAACAGATTAATACCTGGTATGC 783
QY 740 CACGCGTAAACGATGAATGCCAGACGTCGCAAGCATGCTTTCGGGTGCACACCTAAC 799
DB 782 CACGCGTAAACGATGAATGCCAGCTGTTGGGTGCTTGCACCGAGTAGGCGAGCTAAC 723
QY 800 GGATTAGCATTCGCGCTGGGAGTACGCTGCGAAGATTAATACTCAAGGAATTCAGG 859
DB 722 GCTTTGAGCATTCGCGCTGGGAGTACGCTGCGAAGATTAATACTCAAGGAATTCAGG 663
QY 860 GGGCCCGCACAGCGGTGGACATGTGTTTAATTCGAAGCAACGCGCAGAACCTTACCA 919
DB 662 GGGCCCGCACAGCGGTGGACATGTGTTTAATTCGAAGCAACGCGCAGAACCTTACCA 603
QY 920 ACCCTTGACATGGCAGGACCGCTGGAGAGATTTCAGCTTTCGTAAGAGACCTGCACACA 979
DB 602 TCCCTTGACATGGCGTGTATCCAGAGAGATTGGGTGCTCACTTCGGTGGCGGCACACA 543
QY 980 GGTGCTGATGGCTGCTGCTGAGCTGCTGCTGAGATGTTTCGGTTAAGTCCGGCAACGAG 1039
DB 542 GGTGCTGATGGCTGCTGCTGAGCTGCTGCTGAGATGTTTCGGTTAAGTCCGGCAACGAG 483
QY 1040 CGCAACCCACGTCCTAGTTCGACCAATTCAGTTGGGAATCTATGGAATCTGCCGATG 1099
|||||

DB 482 CGAACCCACGCTCTTAGTTCCCATC-ATTCAAGTTGGCACTTAGGAGAGACTGCCGGT 424
QY 1100 ATAAGTCG-GAGGAAGGTGTGATGACGTCAAGTCTCATGGGCTTACGGGTTCGGGCTA 1158
DB 423 ATAAGCCGCGAGGAAGGTGTGATGACGTCAAGTCTCATGGGCTTACGGGTTCGGGCTA 364
QY 1159 CACAGTGTCTACATGGTGTGACAGTGG-----GTTAATCCCC 1197
DB 363 CACAGTGTCTACATGGGCTGACAGTGGGACGCGAAGAGCGATCTCGAGCAATCCCC 304
QY 1198 AAAAGCCATCTCAGTTCGATTGCTCTGCAACTCGAGGCGCATGAAGTTGGAATCGCTA 1257
DB 303 AAAAGCCGCTCAGTTCGATTGCTCTGCAACTCGAGTGCATGGAAGCGGATCGCTA 244
QY 1258 GTAATCGCGGAACAGCATGCGCGGTGAATAGTTCGCGGCTTGTACACACCGCCCGT 1317
DB 243 GTAATCGTGGATCAGCATGCGCGGTGAATAGTTCGCGGCTTGTACACACCGCCCGT 184
QY 1318 CACACCATGGAGTGTGTTCTACCGGACGACGNTGCGCTAACCTTCGGGGGCGAGCGGC 1377
DB 183 CACACCATGGAGTGTGTTCTTACCGGACGCGCTGCGCAACCGCAAGGAGCGAGCGAC 124
QY 1378 CACGTTAGGATCAGGACTGGGTCGAGTCTGTAACAGGTAGCCGTAGGGAACTCGGG 1437
DB 123 CACGTTAGGATCAGGACTGGGTCGAGTCTGTAACAGGTAGCCGTAGGGAACTCGGG 64
QY 1438 CTGGA 1442
DB 63 CTGGA 59

RESULT 13
US-09-894-467-2/c
; Sequence 2, Application US/09894467
; GENERAL INFORMATION:
; APPLICANT: Lindner, Luther E.
; APPLICANT: MacPhee, Kathleen
; TITLE OF INVENTION: Human Blood Bacterium
; FILE REFERENCE: D6026D
; CURRENT APPLICATION NUMBER: US/09/894,467
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/187,946
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 20
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: 58 rRNA sequence of a new human blood bacterium
US-09-894-467-2

Query Match 74.8%; Score 1086.4; DB 37; Length 1502;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches 177; Indels 23; Gaps 3;

QY 20 ACAGACGCTGCGGCGGCTTAAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCGG 79
DB 1502 ACAGACGCTGCGGCGGCTTAAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCGG 1443
QY 80 GGAGGGGTAGTAACGCGTGGGAACGTCCTTCTTACGGAATAGCCCCGGGAAATCGG 139
DB 1442 GGAGGGGTAGTAACGCGTGGGAACGTCCTTCTTACGGAATAGCCCCGGGAAATCGG 1383
QY 140 GAGTAATACCTATACGCGCTTGGGGAAGAGATTATCGAGAGAGATCGCCCGGCTT 199
DB 1382 GGCTAATACCGGATACGCGCTTATGGGGAAGAGATTATCGCCGGAAGATCGCCCGGCTC 1323
QY 200 GGATTAGTAGTGTGGTGGGTAATGGCCCAACGACGACGATCCATAGCTGGTTGAGA 259
DB 1322 TGATTAGCTAGTGTGGTGGGTAATGGCCCAACGACGACGATCCATAGCTGGTTGAGA 1263
QY 260 GGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGGACGAGTGG 319
|||||

Db 1262 GGATGATACCCACATGGGACTGAGACAGCGCCACGACTCTACGGGAGCGACGATGG 1203
QY 320 GGAATCTTAGACAACTGGGCAACCTGATCTAGCCATCGCGGTGAGTGATCAAGGCCT 379
Db 1202 GGAATATTGGACAATGGGCAACCTGATCCAGCCATCGCGGTGAGTGATCAAGGCCT 1143
QY 380 TAGGGTGTAAAGCTCTTTTCAGCTGGGAAGATATGACGGTACACGAGGAAGCCCG 439
Db 1142 TAGGGTGTAAAGCTCTTTTCAGGGAGCAATATGACGGTACCGGAGGAATAGCCCG 1083
QY 440 GCTAACTCCGTCCAGAGCCGCGGTAAATACGAGGGGGGTAGCGTTGTCGGAATACT 499
Db 1082 GCTAACTCCGTCCAGAGCCGCGGTAAATACGAGGGGGGTAGCGTTGTCGGAATACT 1023
QY 500 GGGCGTAAAGCGCAGCTAGCGGACTGGAAGTGCAGAGGTGAATCCACGGGTCAACCT 559
Db 1022 GGGCGTAAAGGGCGGTATCGCGGTTTAAAGTCGGGGTGAAGCCGTGGGCTCAACCA 963
QY 560 TGAAGCTCCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGTGAGTGAATCCGAGTG 619
Db 962 CAGAATGGCCTTCGATACTGGGACGCTWAGATGTTGAGGTGTTGTTGGAATCGAGTG 903
QY 620 TAGAGGTGAATTCGTAGATATTCGAGGAGAACACCACTGCGGAAGCGGGTCACTGGCTC 679
Db 902 TAGAGGTGAATTCGTAGATATTCGCAAGAACACCGGTGCGAAGCGGCGCAACTGGACC 843
QY 680 GATACGACCTGAGTGCAGAAAGCGTGGGAGCAACAGGATAGATACCTGGTGTGTC 739
Db 842 ATTACTGACCTGAGCGCGCAAGCGTGGGAGCAACAGGATAGATACCTGGTGTGTC 783
QY 740 CAGCGCTAAACGATGAATCCAGAGCTGCGAAGCATGCTTGTGCGTGCACACCTAAC 799
Db 782 CAGCGCTAAACGATGAATCCAGCTGTTGGGTGCTTGCACCGCATAGCGAGCTAAC 723
QY 800 GGATTAGCATTCGCGCTGGGAGTACGCTCGCAAGATTAAACTCAAAGGAATGACGG 859
Db 722 GCTTTAGCATTCGCGCTGGGAGTACGCTCGCAAGATTAAACTCAAAGGAATGACGG 663
QY 860 GGGCCGCGACAGCGGTGGAGCATGTTGTTAATCGAAGCAAGCGCGCAACCTTACCA 919
Db 662 GGGCCGCGACAGCGGTGGAGCATGTTGTTAATCGAAGCAAGCGCGCAACCTTACCA 603
QY 920 ACCTTGCATGCGCAGGACCGCTGGAGAGATTGAGCTTCTCTGTAAGAGACCTGCACCA 979
Db 602 TCCTTTGACATGGCGTTTACCAGAGAGATTGGGTCCATTCGGTGGCGCGCACCA 543
QY 980 GGTGCTGCATGGCTGTGTCAGCTGCTGCTGAGATGTTGCGTTAAGTCCGGCAAGAG 1039
Db 542 GGTGCTGCATGGCTGTGTCAGCTGCTGCTGAGATGTTGGGTAAAGTCCCGCAAGAG 483
QY 1040 CGCAACCCAGCTCCTAGTTGCGAGCAATTCAGTTGGGACTCTATGGAACCTGCCGATG 1099
Db 482 CGCAACCCAGCTCCTAGTTGCGCATC-ATTGAGTTGGGACTCTAGGAGAGCTGCCGATG 424
QY 1100 ATAAGTCG-CAGGAAGTGTGGATGAGTCAAGTCCCTCATGGGCTTACGGTTGGGCTA 1158
Db 423 ATAAGTCGCGAGAGAGTGTGGATGAGTCAAGTCCCTCATGGGCTTACGGGATGGGCTA 364
QY 1159 CACAGCTGCTACAAATGGTGTGACAGTGG-----GTTAATCCCC 1197
Db 363 CACAGCTGCTACAAATGGTGTGACAGTGGGAGCGGAGGAGCGATCTGGAGCAATCCCC 304
QY 1198 AAAAGCATCTCAGTTCGGATGTTCTCTGCACTCAGGCGCATGAAGTTGGATCGCTA 1257
Db 303 AAAAGCGCTCAGTTCGGATGTTCTGCACTCAGTTCAGTGCATGAAGGCGGATCGCTA 244
QY 1258 GTATCCGGAACAGCATCGCGGTGAATACGTTCCCGGCTTGTACACACCGCCCGT 1317
Db 243 GTATCCGGAATCAGCATCGCACGGTGAATACGTTCCCGGCTTGTACACACCGCCCGT 184
QY 1318 CACACCATGGAGTGTGTTCTTACCGGACGAGTTCGCTTAACCTTCGGGGGCGGAGCGGC 1377

Db 183 CACACCATGGGACTTGTCTTACCCGACGGCGTGGCCCAACCGCAGGAGGAGCGGAC 124
QY 1378 CAGGTAGGATACGACGACTGGGTGAAGTCTTAACAAGGTAGCCGTAGGGGAACCTGCGG 1437
Db 123 CAGGTAGGTCAGGACGACTGGGTGAAGTCTTAACAAGGTAGCCGTAGGGGAACCTGCGG 64
QY 1438 CTGGA 1442
Db 63 CTGGA 59
RESULT 14
US-09-900-876-2
; Sequence 2, Application US/09900876
; GENERAL INFORMATION:
; APPLICANT: WATANABE, KATSUJI
; APPLICANT: OKUDA, MITSURU
; TITLE OF INVENTION: METHOD AND SYSTEM FOR SEARCHING FOR RELATIONSHIPS BETWEEN B
; FILE REFERENCE: 210847USOX
; CURRENT APPLICATION NUMBER: US/09/900,876
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: JP 2000-215134
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Rhodospirillum rubrum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (72)..(73)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (85)..(85)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (485)..(485)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (490)..(490)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (596)..(596)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (709)..(709)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (828)..(828)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (875)..(875)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (910)..(911)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (988)..(988)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (1045)..(1045)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (1332)..(1333)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (1408)..(1408)
; OTHER INFORMATION: n = c, g, a, or t

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; NAME/KEY: misc_feature
; LOCATION: (1437)..(1442)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (1451)..(1475)
; OTHER INFORMATION: n = c, g, a, or t
US-09-900-876-2

Query Match 71.9%; Score 1044.6; DB 38; Length 1490;
Best Local Similarity 83.9%; Pred. No. 6.1e-303; Indels 31; Gaps 7;
Matches 1941; Conservative 0; Mismatches 208;

Qy 1 AGTTTGATCTCGCTCAGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCG- 59
Db 11 AGTTTGATCTCGCTCAGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCG 70
Qy 60 -AGACCTTCGGGCTCAGCGCGGAGGCTGAGTAACGCTGGGAAAGCTTCCTAC 118
Db 71 ANNCCTTCGGGGTGNAGCGCGGAGGCTGAGTAACGCTGGGAAAGCTTCAGGGCT 130
Qy 119 GGAATAGCCCCGGAAGCTGGGAGTAATACCGTATACGCCCTTTGGGGAAGATTATC 178
Db 131 GGAATAGCTCTGGAAGCGGAGCTAATACCGGATACGCCGTATTGGGAAGAAAT--TC 188
Qy 179 GGAGAGGATCGGCCCGCTTGGATTAGTAGTGGTGGGCTTAATGGCCCAAGCCGA 238
Db 189 GGCTTGGATGGGCCCGCTTGGATTAGTAGTGGTGGGCTTAACGCCCTACCATGGCA 248
Qy 239 CGATCCATAGCTGGTTGAGAGGATGATCAGCACACTGGGACTGAGACAGGCCAGAC 298
Db 249 CGATCCATAGCTGGTTGAGAGGATGATCAGCACACTGGGACTGAGACAGGCCAGAC 308
Qy 299 TCCTACGGGAGGAGCAGTGGGAACTTACAGAACTGGGGCAACCTGATCAGCCATG 358
Db 309 TCCTACGGGAGGAGCAGTGGGAACTTACAGAACTGGGGCAACCTGATCAGCCATG 368
Qy 359 CCAGCTGAGTATGAGGCTTGGGTTGTAAGCTCTTTCAGCTGGGAAAGATAAGACG 418
Db 369 CCAGCTGAGTATGAGGCTTGGGTTGTAAGCTCTTTCAGCTGGGAAAGATAAGACG 428
Qy 419 GTACACAGAGAGAGCCCGGCTAAGCTCGTCCAGCAGCCGCGGTAAATACGGAGGG 478
Db 429 GTACCTCGAAGAGAGCTCCGGTAACTCCGTCAGCAGCCGCGGTAAATACGGAGGG 488
Qy 479 CTAGCGTTGTCGGAATTAAGCTGGAAGCGCAGCTAGCGGAGCTGGAAGTACAGAG 538
Db 489 CNAGCGTTGTCGGAATTAAGCTGGAAGCGCAGCTAGCGGAGCTGGAAGTACAGAG 548
Qy 539 TGAATCCAGGGCTCAACTTGGAACTGCTTTGAACTATCAGTCTGGAGTTCGAGAG 598
Db 549 TGAAGCCCGGGCTCAACTTGGAACTGCTTTGAACTATCAGTCTGGAGTTCGAGAG 608
Qy 599 AGGTGAGTGGAAATCCAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAACACAGTG 658
Db 609 AGGTGAGTGGAAATCCAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAACACAGTG 668
Qy 659 GCGAAGCGGCTACTGGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 718
Db 669 GCGAAGCGGCTACTGGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 728
Qy 719 GGATTAGATACCTTGGTAGTCCAGCGGTAAACGATGAATCCAGAGCTCGGCAAGCAT - 777
Db 729 GGATTAGATACCTTGGTAGTCCAGCGGTAAACGATGAATCCAGAGCTCGGCGCTCTTA 788
Qy 778 GCTTGTGGGTGTCACACCTAACCGATTAAAGCATTCGCCCTGGGGAGTACGGTCCGAAGAT 837
Db 789 GAGTTTGGGTATCCAGCTAACCGATTAAAGCATTCGCCCTGGGGAGTACGGTCCGAAGAT 848
Qy 838 TAAAGCTCAAGGAATTAAGCGGGGCGGCGCAGAGCGGTGGAGCATGTGTTTAATTCGA 897
Db 849 TAAAGCTCAAGGAATTAAGCGGGGCGGCGCAGAGCGGTGGAGCATGTGTTTAATTCGA 908
Qy 898 AGCAACGCGCAGAACCTTACCAACCTTGCATGGCAGGACCGCTGGAGAGATT--CAGC 955

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RESULT 15

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US-10-015-127-578
; Sequence 578, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(13806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 578
; LENGTH: 60918
; TYPE: DNA
; ORGANISM: Sphingomonas elodea
US-10-015-127-578

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Query Match 71.9%; Score 1044.2; DB 44; Length 60918;
Best Local Similarity 84.6%; Pred. No. 3.1e-302;
Matches 1252; Conservative 0; Mismatches 199; Indels 29; Gaps 6;

Qy 1 AGTTTGATCTCGCTCAGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGA 60
Db 16289 AGTTTGATCTCGCTCAGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGA 16348
Qy 61 GA--CCTTCGGTCTAGCGGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 118
Db 16349 GATCCTTCGGGGTCTAGTGGCGCAGCGGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 16408
Qy 119 GGAATAGCCCCGGAAGCTGGGAGTAATACCGTATACGCCCTTTGGGGGAAGATTATC 178

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Result No.	Score	Query Match	Length	DB	ID	Description
1	839.4	57.8	1542	5	US-09-655-378A-158	Sequence 158, App
2	828.6	57.1	1490	6	US-10-465-448-1	Sequence 1, Appl
3	784.6	54.0	1547	1	PGT-US03-20082-16	Sequence 16, Appl
4	776.8	53.5	1555	5	US-09-655-378A-160	Sequence 160, App
5	740.2	51.0	1513	5	US-09-655-378A-159	Sequence 159, App
6	713.6	49.1	1497	6	US-10-367-794A-3052	Sequence 3052, App
7	713.6	49.1	1497	6	US-10-367-794A-3053	Sequence 3053, Ap
8	713.6	49.1	1678	6	US-10-367-794A-2845	Sequence 2845, Ap
9	713.6	49.1	1686	6	US-10-367-794A-12	Sequence 12, Appl
10	713.6	49.1	1686	6	US-10-367-794A-2844	Sequence 2844, Ap
11	713.6	49.1	1686	6	US-10-367-794A-2994	Sequence 2994, Ap
12	713.6	49.1	1686	6	US-10-367-794A-2995	Sequence 2995, Ap
13	699.4	48.2	1522	6	US-10-461-990-1	Sequence 1, Appl
14	662.6	45.6	1102	6	US-10-367-793A-3533	Sequence 3533, Ap
15	662.6	45.6	1108	6	US-10-367-793A-3357	Sequence 3357, Ap
16	662.6	45.6	1108	6	US-10-367-793A-3358	Sequence 3358, Ap
17	662.6	45.6	1108	6	US-10-367-793A-3532	Sequence 3532, Ap
18	662.6	45.6	1132	6	US-10-367-793A-3551	Sequence 3551, Ap
19	657.4	45.3	1262	6	US-10-305-273B-6	Sequence 6, Appl
20	657.4	45.3	1285	6	US-10-305-273B-18	Sequence 18, Appl
21	657.4	45.3	1285	6	US-10-305-273B-19	Sequence 19, Appl
22	657.4	45.3	1287	6	US-10-305-273B-5	Sequence 5, Appl
23	655.8	45.2	1393	6	US-10-305-273B-69	Sequence 69, Appl
24	652.2	44.9	1131	6	US-10-367-793A-3263	Sequence 3263, Ap
25	623.6	42.9	1031	6	US-10-305-273B-56	Sequence 56, Appl
26	623.6	42.9	1031	6	US-10-305-273B-57	Sequence 57, Appl

Db 10 AGTTTATCATGGCTCAGATTGAAGCTGGCGGAGGCTTAACATGCAAGTCGAACGG 69
QY 61 GACC-----TTCCGGTCTAGCGCGGACGGGTGAGTAAACGCTGGGA 102
Db 70 TACAGGAAGAAGCTTCTTCTGCTGACGAGTGGCGGAGGGTGAATGCTGGGA 129
QY 103 AGTGGCCCTTCTACGGAATASCOCGGGAACCTGGGAGTAAATACCGGTATACCGCCTTT 162
Db 130 AACTGCTGATGAGGGGATAACTACTTGGAAACGGTAGCTAATACCGCATACCTCGCA 189
QY 168 GGGGAAGA-----TTTATCGAGAGAGGATCGCGCGGCTTGGATTAGT 208
Db 190 AGACCAAGAGAGGGGACCTTCGGGCTCTTGGCATCGGATGTGCCAGATGGGATTAGT 249
QY 209 AGTTGGTGGGTAAATGGCCACCAAGCGGACCATCATAGCTGTTTGAAGAGATGATCA 268
Db 250 AGTAGTGGGTAAACGGCTACCTAGGGGACCATCCCTAGCTGGTCTGAGAGGATGACCA 309
QY 269 GCCACACTGGGACTGAGACACGCGCCAGACTCTCTACGGGAGGACGAGTGGGGAATCTTA 328
Db 310 GCCACACTGGAATGAGACACGCTCCAGACTCTCTACGGGAGGACGAGTGGGGAATTTG 369
QY 329 GACATGGGGCAACCTGATCTAGCCATGCGCGGTAGTATGAAGGCTTTAGGGTTGT 388
Db 370 CACAATGGGCGCAAGCCTGATGACGACCATGCGCGGTATGAAGAAGGCTTCGGGTTGT 429
QY 389 AAAGCTCTTTACGCTGGGAAGAT-----NATCACGGTACC 423
Db 430 AAAGTACTTTACGCGGGAGGAGGAGTAAAGTTAAATACCTTTGCTCATTCACGTTACC 489
QY 424 AGCAGAAGAAGCCCGGCTAACTCGGTGCCAGCAGCGCGGTAAATACGGAGGGGCTAGC 483
Db 490 CGCAGAAGAAGCACCGGCTAACTCGGTGCCAGCAGCGCGGTAAATACGGAGGGTGAACG 549
QY 484 GTTGTTCGAATTAAGTGGCGTAAAGCGCACAGTGGGAGCTGGAAGTCAAGGTGAA 543
Db 550 GTTAATCGGAATTAAGTGGCGTAAAGCGCACAGTGGGAGCTGGAAGTCAAGGTGAA 609
QY 544 TCCAGGGCTCAACCTTGAACCTGCTTGAACATCATAGTGGGAGTTCGAGAGAGTG 503
Db 610 TCCCGGGCTCAACCTGGAAGTCTGATGACGAGTGGCAAGTTCGATCTCTAGAGGGG 669
QY 604 AGTGAATTCGAGGTAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGCGAA 663
Db 670 GTAGAAATTCAGGTGATCGGTGAATTCGTAGATCTGGAGGAATACCGTGGCGAA 729
QY 664 GCGGGCTACTGCTGATGATGACGCTGAGTGGGAAAGCGTGGGAGCAACAGGATT 723
Db 730 GCGGGCCCTTGACGGAAGACTGACGCTCAGGTGGGAAAGCGTGGGAGCAACAGGATT 789
QY 724 AGATACCCCTGTAGTCCAGCGGTAAACGATCAATGCCAGCTCGGCAAGCATGCTT-G 782
Db 790 AGATACCCCTGTAGTCCAGCGGTAAACGATCAATGCCAGCTCGGCAAGCATGCTT-G 849
QY 783 TCGGTGTCAACCTTAACGGATTAAAGCATTCGCCCTGGGAGTACGCTGCAAGATTAAAA 842
Db 850 TGGCTTCGGAGCTAACGGGTTAAGTCGACCGCTGGGAGTACGCGCGCAAGTTAAA 909
QY 843 CTCAAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGTTTAAATTCGAGCAA 902
Db 910 CTCAAATGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGTTTAAATTCGATGCAA 969
QY 903 CCGCGAAGACCTTACCACCTTGACATGCGAGGACCGCTGAGAGATTACCTTTCG 962
Db 970 CCGAAGAACCTTACCTTGTGATCTCCAGGAGTTTTCAGAGATGAGAAATGTGCT 1029
QY 963 TAAGAGACCTGCACAGGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
Db 1030 TCGGGAACCGTGAAGAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1089
QY 1023 TTAAGTCCGGCAAGAGCGCAACCCAGCTCCCTAGTTCGCCAATATTCAGTTGGGAATC 1082
Db 1090 TTAAGTCCGGCAAGAGCGCAACCCCTTATCTTGTGTCAGCGGTCCGCGCGGCAATC 1149

QY 1083 TATGAAACTGCCGATGATAAGTCGGAGGAGGTGTGGATGACGTCAAGTCTCATGGGC 1142
Db 1150 AAAGGAGACTGCCACTGATAAACTGGAGGAGGTGGGATGACGTCAAGTCTCATGGGC 1209
QY 1143 CTTACGGGTGGGTACACACGCTGTACAAATGGTGGTGACAGTG----- 1186
Db 1210 CTTACGACGAGGCTTACACGCTGTACAAATGGCATCAAAAGAGAGACGACCTCGCA 1269
QY 1187 -----GGTTAATCCCAAAAGCCATCTCAGTTCCGATTCCTCTGCAACTCGAGGCA 1240
Db 1270 GAGCAAGCGGACCTCATAAAGTGCCTAGTCCGAGTTGGAGTCTGCAACTCGACTCCA 1329
QY 1241 TGAAGTTGGAATCGGTAGTAAATCGCGGAACACGATCCGCGTGAATAGTTCCTCCCGGCC 1300
Db 1330 TGAAGTCGAATCGGTAGTAAATCGGTAGTCAAGATGCCAGGTGAATAGTTCCTCCCGGCC 1389
QY 1301 TTGTACACACCGCCGCTCACACATGGGAGTTGGTTTACCCGAGACAGCTGCTAAC 1360
Db 1390 TTGTACACACCGCCGCTCACACATGGGAGTTGGTTTGAAGAGTAGTAGTCTAAC 1449
QY 1361 TTCGGGGGACGCGGCGCACGCTAGATCAGGAGTGGGTTGAAGTCTGTAACAGGTAGC 1420
Db 1450 TTCGGGAGGGCGCTTACCACCTTTGTGATTCATGACTGGGGTGAAGTCTGTAACAGGTAA 1509
QY 1421 CGTAGGGAACCTCGCGCTGAGTACCTCCTT 1452
Db 1510 CGTAGGGAACCTCGCGTTGGATCACCCTT 1541

RESULT 2

US-10-465-448-1

; Sequence 1, Application US/10465448

; GENERAL INFORMATION:

; APPLICANT: Hong Kong University of Science and Technology

; TITLE OF INVENTION: ANTI-FOULING COMPOSITION AND METHOD OF PRODUCTION THEREOF

; FILE REFERENCE: 12069-3

; CURRENT APPLICATION NUMBER: US/10/465,448

; CURRENT FILING DATE: 2003-06-19

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: Patent version 3.1

; SEQ ID NO 1

; LENGTH: 1490

; TYPE: DNA

; ORGANISM: Vibrio proteolyticus or Vibrio alginolyticus

US-10-465-448-1

Query Match

Best Local Similarity 57.1%; Score 828.6; DB 6; Length 1490;

Matches 1106; Conservative 0; Mismatches 275; Indels 63; Gaps 5;

QY 68 GGGTCTAGCGGCGGAGGTGAGTACGGTGGGAGACGTGCCCTTCTTACGGAATAGCC 127
Db 47 GCGTCGAGCGGCGGAGGTGAGTACGTAGGAAATTCGCCCTGATGTGGGGATTAAC 106
QY 128 CCGGAAACTGGGAGTAAATACGCTATACGCCCTTTGGGGAAAGATT----- 174
Db 107 ATTGAACAGTGGCTAATACCGCATGATGCCCTACGGCCCAAGAGGGGAGCCTTCGGGC 166
QY 175 -TATCGGAGAGGATCGGCCCGCTTGGATTAGGTAGTGGTGGGTAATGCCCAACAA 233
Db 167 CTCCTCGCTCAGGATATGCTAGGTGGGATTAGTGGTGGGTAAGGCTCACCAC 226
QY 234 GCCGAGATCCATAGCTGTTTGAAGGATGATGACCACTGGGACTGACACAGCGGC 293
Db 227 GCGGAGATCCCTAGCTGCTGAGAGGATGATGACCCACTGGAACCTGAGACAGGTC 286
QY 294 CAGACTCTTACGGGAGGACGAGTGGGAACTCTTAGACAATGGGCAACCTGTATAG 353
Db 287 CAGACTCTTACGGGAGGACGAGTGGGAACTCTTAGACAATGGGCAACCTGTATAG 346
QY 354 CCATCGCGGTGAGTGAAGGCTTAGGTTGTAAAGCTTTTTCAGCTGGGAAGA--- 410


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QY 533 CAGAGGTGAATCCAGGGCTCAACCTTGAAGTGCCTTTGAACACTATCAGTCGGAGTT 592
D 534 CAGAGGTGAATCCAGGGCTCAACCTTGAAGTGCCTTTGAACACTATCAGTCGGAGTT 593
D 535 CAGAGGTGAATCCAGGGCTCAACCTTGAAGTGCCTTTGAACACTATCAGTCGGAGTT 592
QY 606 CTGCTGTTAAACCCGGGCTCAACTCCGGCTGCATCGAAGAACTGTGACTTGAAGT 664
D 607 CTGCTGTTAAACCCGGGCTCAACTCCGGCTGCATCGAAGAACTGTGACTTGAAGT 664
QY 593 CGAGAGAGGTGAGTGAATCCAGGTCTAGAGTGAATTCGTTAGATATTCGGAGGAACA 652
D 594 CGAGAGAGGTGAGTGAATCCAGGTCTAGAGTGAATTCGTTAGATATTCGGAGGAACA 652
D 595 CGAGAGAGGTGAGTGAATCCAGGTCTAGAGTGAATTCGTTAGATATTCGGAGGAACA 652
QY 665 CAGAGAGGAAAGTGGAAATCCACGTGTAGCGGTGAATTCGTTAGATATTCGGAGGAACA 724
D 666 CAGAGAGGAAAGTGGAAATCCACGTGTAGCGGTGAATTCGTTAGATATTCGGAGGAACA 724
QY 653 CCACTGGCGAAGGCGGCTCACTGGCTGATACCTGACGCTGAGGTGCGAAGCGTGGGGAG 712
D 654 CCACTGGCGAAGGCGGCTCACTGGCTGATACCTGACGCTGAGGTGCGAAGCGTGGGGAG 712
D 655 CCACTGGCGAAGGCGGCTCACTGGCTGATACCTGACGCTGAGGTGCGAAGCGTGGGGAG 712
QY 725 CCACTGGCGAAGGCGGCTCACTGGCTGATACCTGACGCTGAGGTGCGAAGCGTGGGGAG 784
D 726 CCACTGGCGAAGGCGGCTCACTGGCTGATACCTGACGCTGAGGTGCGAAGCGTGGGGAG 784
QY 713 CAACAGAGATAGATACCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 770
D 714 CAACAGAGATAGATACCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 770
D 715 CAACAGAGATAGATACCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 770
QY 785 CAACAGAGATAGATACCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 844
D 786 CAACAGAGATAGATACCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 844
QY 771 CAACAGATGCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 830
D 772 CAACAGATGCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 830
D 773 CAACAGATGCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 830
QY 845 GTTTCGATACCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 904
D 846 GTTTCGATACCTGCTGAGTCCAGCCGTAACAGTGAATGATCCAGACGT--CGG 904
QY 831 GCAAGATTAACACTCAAGGAATGACGGGGGCGGCAAGCGGTGGAGCATGTGTTT 890
D 832 GCAAGATTAACACTCAAGGAATGACGGGGGCGGCAAGCGGTGGAGCATGTGTTT 890
D 833 GCAAGATTAACACTCAAGGAATGACGGGGGCGGCAAGCGGTGGAGCATGTGTTT 890
QY 905 GCAAGACTGAACTCAAGGAATGACGGGGGCGGCAAGCGGTGGAGCATGTGTTT 964
D 906 GCAAGACTGAACTCAAGGAATGACGGGGGCGGCAAGCGGTGGAGCATGTGTTT 964
QY 891 AATTCGAAGCAACGGCGAGAACCTTACCAACCTTGACATGGCGAGGACCGTGGAGAGAT 950
D 892 AATTCGAAGCAACGGCGAGAACCTTACCAACCTTGACATGGCGAGGACCGTGGAGAGAT 950
D 893 AATTCGAAGCAACGGCGAGAACCTTACCAACCTTGACATGGCGAGGACCGTGGAGAGAT 950
QY 965 AATTCGAAGCAACGGCGAGAACCTTACCAACCTTGACATGGCGAGGACCGTGGAGAGAT 1024
D 966 AATTCGAAGCAACGGCGAGAACCTTACCAACCTTGACATGGCGAGGACCGTGGAGAGAT 1024
QY 951 TCAGCTTCTGCTAAGAGACCTGCACACAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTG 1010
D 952 TCAGCTTCTGCTAAGAGACCTGCACACAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTG 1010
D 953 TCAGCTTCTGCTAAGAGACCTGCACACAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTG 1010
QY 1025 TAGGGCTTCCCTCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1084
D 1026 TAGGGCTTCCCTCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1084
QY 1011 TGAGATGCTGCTTAACTCCGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1070
D 1012 TGAGATGCTGCTTAACTCCGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1070
D 1013 TGAGATGCTGCTTAACTCCGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1070
QY 1085 TGAGATGCTGCTTAACTCCGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1143
D 1086 TGAGATGCTGCTTAACTCCGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1143
QY 1071 AGTTGGAGACTCTATGGAATGCGGATGATGATGATGATGATGATGATGATGATGATGAT 1130
D 1072 AGTTGGAGACTCTATGGAATGCGGATGATGATGATGATGATGATGATGATGATGATGAT 1130
D 1073 AGTTGGAGACTCTATGGAATGCGGATGATGATGATGATGATGATGATGATGATGATGAT 1130
QY 1144 AGTTGGGCACTCTAGAGTGAATGCGGCTGACAAACCGGAGGAGGAGGAGGAGGAGGAG 1203
D 1145 AGTTGGGCACTCTAGAGTGAATGCGGCTGACAAACCGGAGGAGGAGGAGGAGGAGGAG 1203
QY 1131 GTCCTCATGCGCTTACGGGTGGGCTACACAGCTGCTACACAGTGTGATGATGATGATGAT 1187
D 1132 GTCCTCATGCGCTTACGGGTGGGCTACACAGCTGCTACACAGTGTGATGATGATGATGAT 1187
D 1133 GTCCTCATGCGCTTACGGGTGGGCTACACAGCTGCTACACAGTGTGATGATGATGATGAT 1187
QY 1204 ATCAATGCTGCTTACGGGTGGGCTACACAGTGTGATGATGATGATGATGATGATGATG 1263
D 1205 ATCAATGCTGCTTACGGGTGGGCTACACAGTGTGATGATGATGATGATGATGATGATG 1263
QY 1188 -----GTTAATCCCAAAAGCCA--TCTAGTTCGGATGCTCTCTG 1228
D 1189 -----GTTAATCCCAAAAGCCA--TCTAGTTCGGATGCTCTCTG 1228
D 1190 -----GTTAATCCCAAAAGCCA--TCTAGTTCGGATGCTCTCTG 1228
QY 1264 GCGAAGCGCGAGGTGGAGCGAATCTTAAAGCGAGTCTCAGTTCGGATTGCGAGGCTG 1323
D 1265 GCGAAGCGCGAGGTGGAGCGAATCTTAAAGCGAGTCTCAGTTCGGATTGCGAGGCTG 1323
QY 1229 AACTCGAGGGCATCAAGTGGATGCTAGTAAATCGCGGAGACACATGCGCGGCTGAATA 1288
D 1230 AACTCGAGGGCATCAAGTGGATGCTAGTAAATCGCGGAGACACATGCGCGGCTGAATA 1288
D 1231 AACTCGAGGGCATCAAGTGGATGCTAGTAAATCGCGGAGACACATGCGCGGCTGAATA 1288
QY 1324 AACTCGGCTGCTGAATGCGGAATGCTAGTAAATCGCGGATCAGCATGCGCGGCTGAATA 1383
D 1325 AACTCGGCTGCTGAATGCGGAATGCTAGTAAATCGCGGATCAGCATGCGCGGCTGAATA 1383
QY 1289 CGTTCCCGGGCTTGTACACACCGCGCTACACATGCGGAGTGGGTTCTACCGGAGCAG 1348
D 1290 CGTTCCCGGGCTTGTACACACCGCGCTACACATGCGGAGTGGGTTCTACCGGAGCAG 1348
D 1291 CGTTCCCGGGCTTGTACACACCGCGCTACACATGCGGAGTGGGTTCTACCGGAGCAG 1348
QY 1384 CGTTCCCGGGCTTGTACACACCGCGCTACACATGCGGAGTGGGTTCTACCGGAGCAG 1443
D 1385 CGTTCCCGGGCTTGTACACACCGCGCTACACATGCGGAGTGGGTTCTACCGGAGCAG 1443
QY 1349 GNTCGGTAACTTCCGGGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1408
D 1350 GNTCGGTAACTTCCGGGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1408
D 1351 GNTCGGTAACTTCCGGGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1408
QY 1444 GGTGGGTAAACCGCAAGGAGGACCGCGGCGGAGGTGGGTAGATGATTGGGGTGAAGTCG 1503
D 1445 GGTGGGTAAACCGCAAGGAGGACCGCGGCGGAGGTGGGTAGATGATTGGGGTGAAGTCG 1503
QY 1409 TAAACAGGTACCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1452
D 1410 TAAACAGGTACCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1452
D 1411 TAAACAGGTACCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1452
QY 1504 TAAACAGGTACCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1547
D 1505 TAAACAGGTACCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1547

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RESULT 4
US-09-655-378A-160
; Sequence 160, Application US/09655378A
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; LYAMICHEV, VICTOR I.
; OLIVE, DAVID M.

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TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
PATHOGENS
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #10, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/655,378A
FILING DATE: 05-Sep-2000
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 1555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-09-655-378A-160

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Query Match 53.5%; Score 776.8; DB 5; Length 1555;
Best Local Similarity 74.1%; Pred. No. 6.8e-242;
Matches 1143; Conservative 0; Mismatches 308; Indels 92; Gaps 9;
QY 1 AGTTTGATCTCTGCTCAGAACGCTGGCGGCGGCTTAACACATCAAGTCGAGCGA 60
D 11 AGTTTGATCTCTGCTCAGAACGCTGGCGGCGGCTTAACACATCAAGTCGAGCGA 70
QY 61 GAC-----CTTCGGGCTACGGCGGAGCGGTGAGTAACGCGTGG--GAA 103
D 71 ACGGACGAGAGAGCTTGTCTCTCTGATGTTAGCGGCGGAGTGAACACGTTGATAA 130
QY 104 CGTCCCTCTCTACGGAATAGCCCGGGAACCTGGGAGTAATACCGTATACGCCCTTGG 163
D 131 CCTACCTATAGACTGGGATAACTTCGGGAACCGGAGCTAATACCGGATATATTTGA 190
QY 164 GGGGAAAGATTATTCGGAGAGAGATCGGC-----CCGCGTTGG 201
D 191 ACCGCATGTTCAAAAGTGAAAGACGGTCTTGTCTCACTTATAGATGATCCGCGTGC 250
QY 202 ATTAGTAGTGTGGTGGTGAATGGCCACCAAGCGGAGCATCCATAGTGTGTTGAGAG 261
D 251 ATTAGTAGTGTGGTGAATGGTGAATGCGGTTACCAAGGCAACGATACGTCGAGAG 310
QY 262 ATGATACGCACTGGGACTGAGACGCGGCGGAGCTCCCTACGGGAGGAGCAGTGGG 321
D 311 GTGATCGGCCACTGGAACCTGAGACGCGTCCCTACGGGAGGAGCAGTGGG 370
QY 322 AATCTTAGACAAATGGGGCAACCTGATCTAGCCATGCGGCTGAGTGAAGAGCCCTTA 381
D 371 AATCTTCGCAATGGCGAAGCCCTGAGGAGCAACGCGCGTGTGATGATGAAGTCTTC 430
QY 382 GGGTTGTAAGCTCTTTCAGCTGGGAAGATAA-----TGA 416
D 431 GGATCGTAAACTCTGTTATTAGGAGAGACATATGTGTAAGTAAGTGTGACATCTTGA 490
QY 417 CGGTACCAGCAGAGAGAGCCCGGCTACTCCGTCGAGCAGCCCGGTAATACGAGGG 476

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Db 491 CGGTACCTTAATCAGAAACCCAGCGCTAACTAGTCCAGCAGCGGTAATACGTAGGT 550
Qy 477 GCCTAGCGTTGTTGGAAATTAATCTAGGCGTAAGAGCCAGTACGCGGACTGGAAGTCAGA 536
Db 551 GCGAAGCGTTATCCGGAAATTAATGGCGCTAAAGCGCGGTAGCGGTTTTAAAGTCTGA 610
Qy 537 GGTGAATCCAGGCGCTCAACCTTGAACCTGCTTTGAACATATAGTCTGAGTTCGAG 596
Db 611 TGTGAACCCACGCTCAACCGTGGAGGTCATTGGAACCTGGAACCTTGAAGTCAGA 670
Qy 597 AGAGGTAGTGAATTCGAGGTGAGAGTGAATTCGTPAGATATTCGAGGAACACCCAG 656
Db 671 AGAGGAAGTGAATTCAGTGTAGTGTAGTGAATTCGCGCAGAGATATGAGGAACACCCAG 730
Qy 657 TGGGAAGCGGCTCAGTGGCTGATCTAGCAGCTGAGTGGGAAAGCGTGGGAGCAAA 716
Db 731 TGGGAAGCGGCTTCTGCTGTAACCTGACGCTGATGTGGAAGCGTGGGATCAAA 790
Qy 717 CAGGATTAGATACCTGTAGTCCACCGCTAAACGATGAATGCCAGAGCTCGGCAAGCA 776
Db 791 CAGGATTAGATACCTGTAGTCCACCGCTAAACGATGAGTGAAGTGTAGGGGGT 850
Qy 777 T--GCTTGTGCTGTCACACCTTAACGGATTAAAGCATTCGCGCTGGGGAGTACGTCGCA 834
Db 851 TCCGCCCTTAGTGTGCTGACGATACGATTAAGCATTCGCGCTGGGGAGTACGACCGCA 910
Qy 835 GATTAAACTCAAGGAATTAACGGGGCCGCAAGCGGTGGAGCATGTGTTTAAT 894
Db 911 GGTGAAACTCAAGGAATTAACGGGGCCGCAAGCGGTGGAGCATGTGTTTAAT 970
Qy 895 CGAAGCAGCGCAACCTTACCAACCTTACATGCGCAGGACCGCTGGAGAGTTCAG 954
Db 971 CGAAGCAGCGCAACCTTACCAACCTTACATGCGCAGGATTCGCAACTTAGAGATAGAG 1030
Qy 955 CTTTCTGCT--AAGAGAGCTGCACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTG 1012
Db 1031 CTTTCTGCTTCCGGGGACAAAGTGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
Qy 1013 AGATGCTGCTTAACTGCGGCAACGAGCGCAACCGCCTAGTGTGCGCAGCAATTCAG 1072
Db 1091 AGATGCTGCTTAACTGCGGCAACGAGCGCAACCGCCTAGTGTGCTGCTGCTGCTG 1149
Qy 1073 TTGGAACTCTATGAACCTGCGATGATGAATGCGGAGAGGTGCTGATGAGTCAAGT 1132
Db 1150 TTGGCACTCTAAGTGTGCTGCGGTCGCAACCGGAGGAGGTGGGATGAGTCAAAAT 1209
Qy 1133 CTTATGCGCTTACGGGTTGGCTACACAGCTGCTACAAATGCTGCTGCTGCTGCTGCTG 1188
Db 1210 CATCATGCTTATGATTTGGGCTACACAGCTGCTACAAATGCTGCTGCTGCTGCTG 1269
Qy 1189 -----TTAATCCCAAAAGCCATCTCAGTTCGAGTTCCTCTCTGCA 1230
Db 1270 GAAACCGGAGGTCAAGCAATCCATAAAGTTGTTCTCAGTTCGAGTTCGATCTGCA 1329
Qy 1231 CTCGAGGCGATGAATGGAATCGCTAGTAAATCGCGGACAGCATCCCGGCTGATACG 1290
Db 1330 CTCGACTACATGAAGTGAATCGCTAGTAAATCGTAGATCAGCATGCTACGGTGAATACG 1389
Qy 1291 TTCGCGGCTTGTACACACCGCGCTACACCATGCGGAGTTCCTACCCGACGACGN 1350
Db 1390 TTCGCGGATTTGTACACACCGCGCTACACCATGCGGAGTTCCTAACCCGACGCGG 1449
Qy 1351 TCGCTAACCTTCGGGGGCG--AGCGGGCCAGCTAGGATCAGGACTGGGGTGAAGTCGT 1409
Db 1450 TGGAGTACCTTTTAGGAGCTAGCCGTCGAGGTGGGACAAATGATTTGGGTGAAGTCGT 1509
Qy 1410 AACAGGTAGCGGTAGGGGAACCTCGGCTGGATCACCTCCCTT 1452
Db 1510 AACAGGTAGCGGTAGGGGAACCTCGGCTGGATCACCTCCCTT 1552

US-09-655-378A-159
; Sequence 159, Application US/09655378A
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; LYAMICHEV, VICTOR I.
; OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; PATHOGENS
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/655,378A
; FILING DATE: 05-Sep-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1513 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 159:
US-09-655-378A-159

Query Match 51.0%; Score 740.2; DB 5; Length 1513;
Best Local Similarity 73.8%; Pred. No. 4.9e-230;
Matches 1114; Conservative 0; Mismatches 329; Indels 67; Gaps 11;
Qy 1 AGTTTGATCTGCTCAGAGCAAGCGCTGGCGGAGGCTTAACACATCAAGTCGAGCGA 60
Db 12 AGTTTGATCTGCTCAGAGCAAGCGCTGGCGGAGGCTTAACATACATCAAGTCGAGCA 71
Qy 61 GACCTTCG-----GGTCTACGCGGAGCAGGCTGAGTGAACGCGTGGG-AA 103
Db 72 TGAAGCTTCTAGCTTGTAGAGTGGATTAGTGGCGCAGCGGTGAGTAGGTATAGTTAA 131
Qy 104 CGTCCCTTCTCTACGGAATAGCCCGGGAAGTGGGAGTAAATACCGTATACGCGCTTT- 162
Db 132 TCTCCCTTACACAGAGGACCAAGTTGGAAACGACTGCTATATCTATCTATCTCTGCTT 191
Qy 163 -----GGGGAAAGATTATCGGAGAAGATCGGCCCGCTGGATTAGGTAG 210
Db 192 AACACAAGTTCAGTAGGAAAGTTTTTCGGTGTAGGATGAGACTATATAGTATCAGTAG 251
Qy 211 TTGTTGGGTAAATGGCCCAACCAAGCCGACGATCCATAGCTGTTTGGAGGATGATCAGC 270
Db 252 TTGTAAGGTAATGGCTTACCAAGGCTATACGCTTAAGTCTGTCTGAGAGGATGATCAGT 311
Qy 271 CACACTGGGACTGAGACACGCGCCAGACTCTACGGGAGGAGGAGGAGTGGGATCTTAGA 330
Db 312 CACACTGGAAGTACGACGCTCCAGACTCCCTACGAGGAGGAGGAGGAGTGGGATCTTAG 371
Qy 331 CAATGGGGCAACCTGATCTAGCCATGCGCGGTGAGTGAAGGAGGAGGAGGAGTGGGAT 390
Db 372 CAATGGGGCAACCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 431


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Db 982 AAGCAACCGGAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGGC 1041
Qy 956 TTTCTGTAAGAGACCTGCACACAGGTGCTGCATGGGTGTGCTGAGTCTGCTGCTGAGA 1015
Db 1042 TTTC-CUTTCGGGACAGAGGTGACAGGTGGTGCATGGTGTGCTGAGTCTGCTGCTGAGA 1100
Qy 1016 TGTTCGGTTAGTCCGCAACGAGCGCAACCCAGTCCCTAGTTTGGCCAGCAATTCAGTTG 1075
Db 1101 TGTTCGGTTAGTCCGCAACGAGCGCAACCCCTATTGTTAGTTGCCATC-ATTAGTTG 1159
Qy 1076 GGAACCTCTATGGAACCTCCGATGATAAGTCCGAGGAGGTGTGATGACGTCAAGTCT 1135
Db 1160 GGCACCTAGCGAGAGTCCCGGTAAATAAACCGGAGGAGGTGGGATGACGTCAATCAT 1219
Qy 1136 CATGGCCCTTACGGGTGGGTACACAGCTGCTACATGG-----TGACG 418
Db 1220 CATGCCCTTATGACCTGGGTACACAGTCTGCTAATGGTGTGCTGACAGTCCGCAAG 1279
Qy 1176 -TGTGACAGTGGGTAAATCCCAAGGCA-TCTCAGTTCGGATTGCTCTGCACTC 1233
Db 1280 CCGGTGACGCGCAAGCTAATCTTTAAAGCCAGTCTCAGTTCGGATTGAGCTGCACTC 1339
Qy 1234 GAGGCGATGAAGTTGGATCGCTAGTAAATCGGGAACAGCATGCCCGGTGAATACGTTT 1293
Db 1340 GCCTACATGAAGTCGGAATCGTAGTAATCGGGATCAGACCGCGGTGCAATACGTTT 1399
Qy 1294 CCGGCGCTTGTACACACCGCGCTACACACATGGGAGTTGTTTACCCGACGACGNTGC 1353
Db 1400 CCGGCGCTTGTACACACCGCGCTACACACGAGAGTTTGAACACCCGAGTGGTGA 1459
Qy 1354 CTAACCTTCGGGGGAGCGGCCCGCTAGGAT 1388
Db 1460 GGTAAACCTAAGGAGCCAGCCGCTAAGTGGGAT 1494

RESULT 8
US-10-367-794A-2845
; Sequence 2845, Application US/10367794A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Streptococcus pneumoniae complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,794A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 3245
; SOFTWARE: Proprietary
; SEQ ID NO 2845
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae complete genome.
; FEATURE:
; LOCATION: (1813570)...(1815247)
; OTHER INFORMATION: Chromosome - 1 Strand - negative ConnectonObjectNumber - 3472
US-10-367-794A-2845

Query Match 49.1%; Score 713.6; DB 6; Length 1678;
Best Local Similarity 73.9%; Pred. No. 2.2e-221;
Matches 1090; Conservative 0; Mismatches 295; Indels 90; Gaps 11;

Qy 1 AGTTTGATCTGGCTCAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
Db 204 AGTTTGATCTGGCTCAGAACGACGCTGGCGGAGGCTTAACATGCAAGTGAACGC 263
Qy 61 -----GACCTTCGGGTCTAGCGCGGAGCGGTGAGTAACGCGT-GGGAACG 105
Db 264 TGAAGGAGGAGCTGCTCTCTGATGAGTTGGACGCGGTGAGTAACGCGTAGTAACC 323
Qy 106 TGCCCTTCTACGGAATAGCCCGGGAACCTGGGAGTAATACGCTATACGCCCTTTGGG 165
Db 324 TGCTCTGAGCGGGGATAACTATTGGAAACGATAGCTAATACCGCATAGAGTAGATGT 383
Qy 166 GGAAGATTTATCGGAGAG-----GATCGGCGCGGTGGATT 204
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Db 384 TGCAATGACATTTGCTTAAAGGTGCATCTGATCCTACCTACAGATGAGCTCGTTGTATT 443
Qy 205 AGGTAGTTGGTGGGGTAAATGCCCCAACAGCCGAGCATCCATAGCTGTTTGGAGAGTATG 264
Db 444 AGCTAGTTGGTGGGGTAAAGGCTCACCAGGCGAGCATACATAGCCGACCTGAGAGGTG 503
Qy 265 ATAGCCACACTGCGGACTGAGACAGCGGCCAGACTCCCTACGGAGGAGCGAGTGGGGAAT 324
Db 504 ATCGGCCACACTGGGACTGAGACAGCGGCCAGACTCCCTACGGAGGAGCGAGTGGGGAAT 563
Qy 325 CTTAGCAATAGGGGCAACCTGATCTAGCCATGCCGCTGAGTGTAGTGAAGGCCCTTAGGG 384
Db 564 CTTGGCAATAGCGAGAGTCTGACCGAGCAACGCGCTGAGTGAAGAAGGCTTTTCGGA 623
Qy 385 TTGTAAGCTCTTTCAGCTGGGAAGATAA-----TGACG 418
Db 624 TCGTAAGCTCTGTTGTAAGAGAGAACGAGTGTGAGAGTGGAAAGTTTCACACTGTGAGG 683
Qy 419 GTACAGCAGAGAGAGCCCGCTAACTCCGTGCCAGCAGCGCGGTAAATACGGAGGGG 478
Db 684 GTATCTACCAAGAGGAGCGCTAACTACGTGCCAGCAGCGCGGTAAATACGTAGTCC 743
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Db 744 CGAGCGTTGTCGGGATTTATTGGCGTAAAGCGAGCGAGCGGTAGTAAGTCTGAAG 803
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Qy 599 AGGTGAGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAGAACACAGTG 658
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Db 1103 TTGAACCTCAAAGGAATTAAGCGGGGCGCGCAAGCGGTGGAGCATGTGTTTAAATCG 1162
Qy 897 AAGCAACCGCAGAACCTTACCACCCCTTGACATGCG-AGGACCGCTGGAGAGATTCAGC 955
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Db 1401 CATGCCCTTATGACCTGGGTGATACAGCTGTGCTAATGGCTGTGACACAGTCCGAAG 1460
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QY 1229 AACTCGAGGCGATGAAGTTGGAATCGCTAGTAAATCGGGAAACAGACAGTCCCGGTGAATA 1288
Db 864 AACTCGACTCCATGAAGTCGGATCGCTAGTAAATCGTGGATCAAGATGCCACCGTGAATA 923
QY 1289 CGTTCGCGGCGCTTGTACACACCGCGGTACACACATGGAGTGGTGTCTACCCGAGAC 1348
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QY 1349 GNTGCGGTAACTTCGGGGGCGAGGCGGCGGAGTGGATGATGATGATGATGATGATGATG 1408
Db 984 GGTAGCTTAACCTTCGGGAGGCGCTTACCACTTTGTGATCATGATGATGATGATGATG 1043
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Db 1044 TAACAAGGTAACTGAGGAAACCTCGCGGTGGATCACTTCCTT 1087

RESULT 15
US-10-367-793A-3357
; Sequence 3357, Application US/10367793A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome with
; FILE REFERENCE: Jim Zeigler Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,793A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 4126
; SOFTWARE: Proprietary
; SEQ ID NO 3357
; LENGTH: 1108
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome with
; FEATURE:
; LOCATION: (4033574)...(4034681)
; OTHER INFORMATION: Chromosome - 1 Strand - positive ConnectionObjectNumber = 4477
US-10-367-793A-3357

Query Match 45.6%; Score 662.6; DB 6; Length 1108;
Best Local Similarity 78.1%; Pred. No. 6.3e-205;
Matches 831; Conservative 0; Mismatches 210; Indels 23; Gaps 2;

QY 412 ATGACGGTACAGCAGAGAGAGAGCCCGGCTAACTCCGTCCACAGCAGCCGCGTAAATACG 471
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QY 472 GAGGGGCTAGGCTTCTCGGATTAATCGGAATTAATCGGCGTAAAGCGCAGTAGGCGGACTGGAAG 531
Db 84 GAGGGTGCAGCGGTTAATCGGAATTAATCGGCGTAAAGCGCAGTAGGCGGCTTGTGTAAG 143
QY 532 TCAGAGGTGAATCCAGGGCTCAACTTGGAACTGCCTTGAAGTATATCAAGTCTGAGT 591
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QY 592 TCGAGAGAGGTGAGTGAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAAC 651
Db 204 CTCGTAGAGGGGGTAGAATCCAGGTGTAGCGTGAATTCGTAGATCTGGAGGAAT 263
QY 652 ACCAGTGGCGAGGCGGCTACATCGCTGATGATGATGATGATGATGATGATGATGATGATG 711
Db 264 ACCGTGGCGAGGCGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 323
QY 712 GCAACAGGATTAAGTATACCTTGTAGTCCACCGCTTAAACGATGATGATGATGATGATGATG 771
Db 324 GCAACAGGATTAAGTATACCTTGTAGTCCACCGCTTAAACGATGATGATGATGATGATGATG 383
QY 772 AAGCATG-CTTGTGCGTGTACACCTAACCGATTAAAGCATTCGCGCTGGGAGTACGGTC 830
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Db 384 GCCTTTGAGCGTGGCTTCGCGAGCTAACGGTTAAGTCGACCCCTTGGGAGTACGGCC 443
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QY 951 TCAGCTTTTCGTAAGAGAGCTGCACACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTG 1010
Db 564 GAGAATGTGCTTCGCGGAAACCGTGTGAGACAGTGTGCTGCTGCTGCTGCTGCTGCTG 623
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QY 1187 -----GTTTAAATCCCAAAAGCCATCTCAGTTCGGATTGCTCTGTC 1228
Db 804 GCGACCTCGGAGAGAGAGCGGACCTATAAAGTGGTCTGCTAGTCCGATTGGAGTCTGC 863
QY 1229 AACTCGAGGCGATGAAGTTGGAATCGCTAGTAAATCGGGAAACAGACATGCCGCGTGAATA 1288
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QY 1289 CGTTCGCGGCGCTTGTACACACCGCGCTCACACCATGGGAGTGGTGTCTACCCGAGCAG 1348
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QY 1349 GNTGCGCTAACTTCGCGGGGCGAGGCGGCGCAGCGTAGGATCAGCGACTGGGGTGAATCG 1408
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QY 1409 TAACAAGGTAGCGGTAGGGAACCTCGCGCTGGATCACTTCCTT 1452
Db 1044 TAACAAGGTAACTGAGGGAACCTCGCGGTGGATCACTTCCTT 1087
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Search completed: July 28, 2003, 12:55:52
Job time : 178 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 09:18:53 ; Search time 2887 seconds

(without alignments)

12223.796 Million cell updates/sec

Title: US-10-049-228-1

Perfect score: 1452

Sequence: 1 agttgatctctggtcgaa.....tgcggctggatcaactctctt 1452

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estl:*

9: gb_estl:*

10: gb_est2:*

11: gb_estc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
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2	686.8	47.3	899	29	BZ685785 PUBDT54TD
3	591.4	40.7	1010	29	BZ431523 BONHD88TF
4	588.8	40.6	1053	29	BZ447500 BONKF40TR

C	5	587.2	40.4	1016	29	BZ426201
C	6	582.8	40.1	1079	28	BH705272
C	7	581.6	40.1	1069	29	BZ474941
C	8	580.2	40.0	1106	29	BZ469058
C	9	566.6	39.0	1084	29	BZ439740
C	10	563.4	38.8	974	29	BZ440868
C	11	557.6	38.4	1077	29	BZ450751
C	12	557	38.4	1054	28	BH647750
C	13	549.8	37.9	1031	28	BH656222
C	14	536	36.9	1044	29	BZ463550
C	15	535	36.8	995	28	BH700021
C	16	534	36.8	947	29	BZ464837
C	17	531.8	36.6	1051	29	BZ494182
C	18	530.4	36.5	1082	29	BZ459110
C	19	520.4	35.8	1020	28	BH685417
C	20	510.4	35.2	1096	29	BZ502068
C	21	506.4	34.9	889	29	BZ426275
C	22	506.2	34.9	862	28	BH527452
C	23	505.4	34.8	1143	28	BH814966
C	24	500.2	34.4	875	28	BH547523
C	25	499.6	34.4	857	28	BH578853
C	26	497	34.2	848	28	BH730827
C	27	496.8	34.2	951	28	BH651765
C	28	496.8	34.2	955	29	BZ486137
C	29	494.6	34.1	977	29	BZ459292
C	30	492.8	33.9	861	28	BH582045
C	31	491.8	33.9	623	14	CD211316
C	32	489.4	33.7	970	29	BZ494246
C	33	487.2	33.6	1030	29	BZ463792
C	34	487	33.5	823	29	BZ498828
C	35	486.8	33.5	823	28	BH573967
C	36	485.4	33.4	865	28	BH453601
C	37	484.8	33.4	616	10	BZ356988
C	38	481.6	33.2	845	28	BH564435
C	39	480.8	33.1	833	28	BH540327
C	40	479.2	33.0	834	29	BZ449239
C	41	478.8	33.0	986	29	BZ490055
C	42	478.4	32.9	935	29	BZ468986
C	43	477	32.9	901	29	BZ461852
C	44	475.6	32.8	861	29	BZ464776
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ALIGNMENTS

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BH771024
LOCUS
DEFINITION
LLGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
ACCESSION
BH771024
VERSION
BH771024.1 GI:20373981
SOURCE
GSS.
ORGANISM
Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
REFERENCE
1 (bases 1 to 6499)
AUTHORS
Bolotin, A., Ehrlich, S.D. and Sorokin, A.
TITLE
Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL
Sci. Aliments, (2002) In press
COMMENT
Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is ywga (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.

FEATURES

source

Location/Qualifiers
1. 6499
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/strain="Mg1363"
/db_xref="taxon:1359"
/clone_lib="Mg1363 Random Sequence Tag Library"
/note="Vector: pSGM2; Site 1: SmaI; Library of
chromosomal fragments of L. lactis strain Mg1363 was
prepared by partial AluI digestion or by sonication."
BASE COUNT * 1946 a 1228 c 1683 g 1642 t
ORIGIN

Query Match 53.4%; Score 776; DB 28; Length 6499;
Best Local Similarity 73.7%; Pred. No. 1.5e-202;
Matches 1134; Conservative 0; Mismatches 316; Indels 89; Gaps 8;
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RESULT 2

BZ685785/c
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genomic survey sequence.
ACCESSION BZ685785
VERSION BZ685785.1 GI:28245311
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 899)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick
A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished
COMMENT Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtowntigr.org
DNA is from a doubled haploid provided by Tom Osborn
Seq primer: T₁
Class: sheared ends.

FEATURES	Location/Qualifiers
source	1. .1079

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/clone_lib="BO_2_3_KB"
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BASE COUNT
ORIGIN
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genomic DNA inserted into pHOS1 using BstXI linkers"

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Query Match 40.1%; Score 582.8; DB 28; Length 1079;
Best Local Similarity 75.5%; Pred. No. 1.3e-149;
Matches 763; Conservative 0; Mismatches 242; Indels 5; Gaps 3;

[illegible]

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Qy	1020	CGGTTAAGTCCGGCAGAGCGCAACCCAGTCCCTAGTTGCCAGCAATTCAGTTGGGAA	1079
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DEFINITION	BONKR59FR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONKR59, genomic survey sequence.		

ACCESSION	B2474941
VERSION	B2474941.1
KEYWORDS	GI:26776372 GSS.
SOURCE	Brassica oleracea
ORGANISM	Brassica oleracea
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids I; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 1069)
AUTHORS	Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
TITLE	Whole genome shotgun sequencing of Brassica oleracea
JOURNAL	Unpublished
COMMENT	Other_GSSs: BONKR59TF Contact: Chris Town
	TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

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FEATURES             Location/Qualifiers
     source            .
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             /organism="Brassica bleracea"
             /mol_type="genomic DNA"
             /strain="TO1000DH3"
             /db_xref="taxon:3712"
             /clone="BONKE59"
             /clone_lib="BO_1.6.2_KB_tot"
             /note="Vector: PHOS1; Site_1: BstXI; 1.6-2 kb sheared
                    total DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT           200 a    351 c    248 g    270 t
ORIGIN

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Query Match	40.1%	Score 581.6;	DB 29;	Length 1069;
Best Local Similarity	74.4%	Pred. No. 2.8e-149;		
Matches 786;	Conservative	0;	Mismatches 264;	Indels 6;
				Gaps 4;

Qy	1	AGTTTGATCTCGCTCAGAACGACGTCGCGCAGGCTTAAACATGCAAGTCGAGCGA	60
Db <td>1056</td> <td>AGTTCGATCTCGCTCAGGATGAACGTCGCGGCATGCTTACACCATGCAAGTCGGACGG</td> <td>997</td>	1056	AGTTCGATCTCGCTCAGGATGAACGTCGCGGCATGCTTACACCATGCAAGTCGGACGG	997
Qy <td>61</td> <td>GACCTTCGGG-TCTAGCGGCGGACGGGTGAGTAACGCGTGGGACGTCGCCCTCTCTACG</td> <td>119</td>	61	GACCTTCGGG-TCTAGCGGCGGACGGGTGAGTAACGCGTGGGACGTCGCCCTCTCTACG	119
Db <td>996</td> <td>GAAGTGGTGTTTCCAGTGCGGGACGGGTGAGTAACGCGTAAAGACCTGCCCTTGGGAGGG</td> <td>937</td>	996	GAAGTGGTGTTTCCAGTGCGGGACGGGTGAGTAACGCGTAAAGACCTGCCCTTGGGAGGG	937

QY	120	GAATAGCCCGGAAACTCGGAGTAATACCGTATACGCCCTTTGGGGGAAAGTAATAT-C	178
Db	936	GAACACCGAGTGGAAACGGCTGCTGCTAATACCCCTAGGCTGAGGAGCAAAAGGAGGAATCC	877
QY	179	GGAGAAGGATCGGCCCGCTGTGATTAGGTAGTTGGTGGGTAATCGCCACCAACGCCGA	238
Db	876	GCCCGAGGAGGGCTCGCGTCTGATTAGCTAGTTGGTAGGCAATAGCTTACCAAGCGCA	817
QY	239	CGATCCATAGCTGGTTGAGAGGATGATCAGGCACACTTGGGACTGAGACACGCCCCAGAC	298
Db	846	TGATCAGTAGCTGTCGAGAGGATGATCAGCCACACTTGGACTGAGACACGSCCCAGAC	757
QY	299	TCCTACGGGAGGACAGATGGGGAACTTATAGACAATGGGGGCAACCTGATCTAGCGATG	358
Db	756	TCCTACGGGAGGACAGATGGGGAAATTTCCGCAATGGCGAAAGGCTGACGAGCAATG	697
QY	359	CCCGTGTAGTATGAAGGCTTAGGTTGTAAAGCTCTTTCAGCTCGGAGA--TAATGA	416
Db	696	CCCGTGTAGGTAGAAGGCTTACGGGTCTTGAACCTCTTTCCAGAGAAGAAGCAATGA	637
QY	417	CGGTACACAGAGAAGACCCCGCTAACTCCCTGCGCAGCAGCGCGGTATATACGGAGG	476
Db	636	CGGTATCTGGGAAATAGCATCGGCTAATCTGTGCCAGCAGCGCGGTATACAGAGGA	577
QY	477	GGCTAGCGTTGTTTCGGAATTTACTGGCGTAAAGCGCACGTPAGCGGACTGGAAAGTCAGA	536
Db	576	TGCAAGCGTTATCCGGAATGATTGGCGTAAAGCGTCTGTAGTTGGCTTTTAAAGTCCGC	517
QY	537	GGTGAATCCCGAGGCTCAACTTGAATGCTCTTTGAAACTATATAGTCTGGAGTTCGAG	596
Db	516	CGTCAATCCCGAGGCTCAACCTTGGACAGCGCGTGGAACTACCAAGCTTGTAGTACGGT	457
QY	597	AGAGGTGAGTGGAAATTCGAGTGTAGAGGTGAATTCGTAGATATTTCGGAGGAAACACCAG	656
Db	456	AGGGCAGAGGGAATTTCCGGTGGAGCGGTGAATTCGGTAGAGATCGGAAGAACACCAA	397
QY	657	TGCGAAGCGGCTCACTGGCTCGATCTAGCAGCTGAGGTGCGAAGACGTTGGGAGCAAA	716
Db	396	CGCGAAAGCACCTCTGCTGGGCGGACACTGACACTGAGAGACGAAAGCTAGGGGAGCGAA	337
QY	717	CAGGATTAGATACCTTGGTAGTCCAGCCGTAACGNTGAATGCCAGACG--TCGGCAAG	774
Db	336	TGGGATTAGATACCCAGTAGTCTTACGCGTAACGATGGATATACTAGGCCCTGTGGGTAT	277
QY	775	CATGCTGTGCTGTACACACTTAACGATTAAAGCATTCGCCCTGGGAGTACGGTCCGAA	834
Db	276	CGACCCGTGAGTGTCTAGCTAACCGGTTAGTATCCCGCCTGGGAGTACGTTCCGAA	217
QY	835	GATTAAACTCAAAGGAATTTACGGGGGCCCCGACAAAGCGGTGAGGACATGTGTTTAATT	894
Db	216	GAATGAAACTCAAAGGAATTTACGGGGGCCCCGACAAAGCGGTGAGGATGTGTTTAATT	157
QY	895	CGAAGCAACCGCAGAACCTTACCACCCCTTGACATGGCAGGACCGCTGAGAGATTCAG	954
Db	156	CGATGCAAGCGGAAGAACCTTACAGGGCTTGACATGGCCCGAATCCCTCTTGAAGAGAG	97
QY	955	CTTTCTCGTAGAGACCTGCACACAGTGTGATGGCTGCTCGTCAAGCTCGTCTCGTGAG	1014
Db	96	GGGTGCTCTCGGGAACGCGGACACAGGTGGTGCATGGCTCTCGTCAAGCTCGTGCCGTAG	37
QY	1015	ATGTTGGTTAACTCGCGCAACGAGGCGCAACCCAGC	1050
Db	36	GTATTGGGTTTAAGTCCCGCAACGAGCGCAACCCCTCG	1

RESULT 8	BZ469058	1106 bp	DNA	linear	GSS 13-DEC-2002
BZ469058/c	BONH954TF	BO_1.6_2_KB_tot	Brassicaceae	genomic clone	BONH54,
LOCUS	genomic survey sequence.				
DEFINITION	BZ469058				
ACCESSION	BZ469058				
VERSION	BZ469058.1	GI:26764665			
KEYWORDS	GSS				

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SOURCE          Brassica oleracea
ORGANISM        Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE       1 (bases 1 to 1106)
AUTHORS         Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M..
TITLE           Whole genome shotgun sequencing of Brassica oleracea
JOURNAL         Unpublished
COMMENT         Other_GSSs: BONHE54TR
                Contact: Chris Town
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA.
                Tel: 301-838-3523
                Fax: 301-838-0208
                Email: cdtown@tigr.org
                DNA is from a doubled haploid provided by Tom Osborn.
                Seg primer: TF
                Class: sheared ends.
FEATURES             Location/Qualifiers
                    1..1106
                        /organism="Brassica oleracea"
                        /mol_type="genomic DNA"
                        /strain="Tc01000DH3"
                        /db_xref="taxon:3712"
                        /clone="BONHE54"
                        /clone_lib="BO_1.6_2_KB_tot"
                        /note="Vector: pHOSI; Site_1: BstXI; 1.6-2 kb sheared
                        total DNA inserted into pHOSI using BstXI linkers"
BASE COUNT       211 a      360 c      255 g      280 t
ORIGIN

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Query Match	40.0%	Score 580.2	DB 29	Length 1106	
Best Local Similarity	74.9%	Pred. No. 6.8e-149			
Matches 792	Conservative	0	Mismatches 258	Indels 7	Gaps 5
QY	1	AGTTTGATCCTGGCTCAGAACACGCTGGCGGCAGCGTTAACACATGCAAGTCGAGCGGA	60		
DB	1077	AGTTTCGATCTGGCTCAGGATGACCGGTGGCGGCATGCTTAACACATGCAAGTCGGACGG	1018		
QY	61	GACCT-TCGGGCTTAGCGGGCGGACGGGTGAGTAACGGGTGGGAACGTCGCCCTTCTCTACG	119		
DB	1017	GAAGTGGTGTTTCCAGTGGCGGACGGGTGAGTAACGGGTGAGTAACGGGTGAGTAACCTTCCGAGG	959		
QY	120	GAATAGCCCCGGGAAACTGGGAGTAATACCGGTATACGCCCTTTGGGGGAAGAGTTAT-C	178		
DB	958	GACACCCAGCTGGAACCGGTGCTTAATACCCCGTAGGCTGAGGAGCAAAAGAGGAGAAATCC	899		
QY	179	GGACAAAGATCGGCCCGCGTGGATTAGGTAGTTGGTGGGTAAATGCCCCACCAAGCGGA	238		
DB	988	GCCCGAGAGGGGCTCGCGTCTGATTAGTGTGGTAGGCAATAGCTTACCAAGCGGA	839		
QY	239	CGATCCATAGCTGCTTTGAGAGGATGATACGCCACACTGGGACATGAGACAGCGGCCAGAC	298		
DB	838	TGATCAGTAGCTGCTCCGAGAGGATGATACGCCACACTGGGACATGAGACAGCGGCCAGAC	779		
QY	299	TCTTACGGGAGGCAGCAGTGGGGAATCTTAGACAATGGGGCAACCTGTATCTAGCCATG	358		
DB	778	TCTTACGGGAGGCAGCAGTGGGGAATTTTCGCAATGGCGAAACGCTGACGGAGCAATG	719		
QY	359	CCGCGTGAGTGATCAAGSCCTTAGGGTTGTAAGCTCTTTCAGCTGGGAAGA--TAATGA	416		
DB	718	CCGCGTGAGGTAGAAGGCTTACGGGCTCGGCTGAACTCTTTTCCAGAGAAAGACCAATGA	659		
QY	417	CGGTACCCAGCAGAAAGCCCGGCTAACTCCGTGCCAGCAGCCCGCGTAAATACGGAGGG	476		
DB	658	CGGTATCTGGGAATAAGCATCGGTAACTCTGTGCCAGCAGCCGCGTAAATACAGAGGA	599		
QY	477	GGCTAGCGTGTCTCGGAATTAATCTGGCGGTAAAGCGCAGCTAGGCGGACTGGAAGATCAGA	536		
DB	598	TGCAAGCGTTATCCGGATGATATGGGCGTAAAGCGTCTGTAGTGGCTTTTTTAAGTCGCG	539		
QY	537	GGTGAATCCCGAGGSCCTCAACCTTGGAACTGCCCTTTGAAACTATTCAGTCTGGAGTTCGAG	596		


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Db      965  GGTCCGATCCCGGAGGTGAGTAACTCAAAAACCCGCTCCCTAGTCGGATTGCAGG 1024
QY      1225  CTCCAACTCGAGGAGTGAATTTGGATCGCTAGTAAATCGCGG 1267
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1025  CTCCAACTCGCTGATGAAGCCGGAATCGTATGATCGCG 1067

RESULT 10
BZ440868
LOCUS      BZ440868                974 bp    DNA        linear    GSS 13-DEC-2002
DEFINITION *BONK51NR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONK51,
genomic survey sequence.
ACCESSION BZ440868
VERSION   BZ440868.1 GI:26698161
KEYWORDS  GSS.
SOURCE    Brassica oleracea
ORGANISM  Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 974)
AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE     Whole genome shotgun sequencing of Brassica oleracea
JOURNAL   Unpublished
COMMENT   Other_GSSs: BONK51TF
          Contact: Chris Town
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA.
          Tel: 301-838-3523
          Fax: 301-838-0208
          Email: cdtown@tigr.org
          DNA is from a doubled haploid provided by Tom Osborn.
          Seq primer: TR
          Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..974
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:3712"
                     /clone_lib="BONK51"
                     /clone_lib="BO_1.6_2_KB_tot"
                     /note="vector: PHOS1; Site_1: BstXI; 1.6-2 kb sheared
                     total DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT      245 a      227 c      314 g      188 t
ORIGIN

Query Match      38.8%; Score 563.4; DB 29; Length 974;
Best Local Similarity 76.7%; Pred. No. 2.8e-144;
Matches 728; Conservative 0; Mismatches 216; Indels 5; Gaps. 3;

QY      231  CAAGCCAGCATCCATAGCTGTTGAGAGATGATCAGCCACACTGGGACTGAGACAG 290
Db      21   CCAGGCGTATGATCAGTACGTGGTCCGAGAGATGATCAGCCACTGGGACTGAGACAG 80
QY      291  GCCCAGACTCTACGGGAGCAGCAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATC 350
Db      81   GCCCAGACTCTACGGGAGCAGCAGTGGGGAATTTCCCAATGGGGCAACCCCTGATC 140
QY      351  TAGCATGCGCGTACGTATGATGAGGCTTAGGCTTAGGCTTAAAGCTCTTTCAGCTGGGAAGA 410
Db      141  GAGCAATGCCGCGTGGAGGTAGAGGCTCAGGGCTCTGAACTCTTTTCCACAGAGA 200
QY      411  --TAATGACGTACACAGAGAAGCCCGGCTAACTCGGTGCCACAGCCGCGGTAAT 468
Db      201  AGCAATGACGGTATCTGGGAATTAAGCATCGCTTAATCTGTGCCAGACCGCGGTAAT 260
QY      469  ACGGAGGGGCTAGCGTTGTTCCGGAATTAATCTGGCGTAAAGCGCACCTAGGCGGACTGGA 528
Db      261  ACAGAGATCAAGCGTTATCCGGAATGATGGCGTAAAGCGTCTGTAGTGCGCTTTT 320
QY      529  AAGTCAGAGTGTAATCCCGAGGCTCAACCTTGAAGTGCCTTTGAACATATCATGTGG 588
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Db      321  AAGTCCCGCTCAAAATCCAGGCTCAACCTCGACAGGCGGTGGAANAACCTACCAAGCTTG 380
QY      589  AGTTTCGAGAGAGTGGAGTAAATTCGAGTGTAGAGGTGAAATTCGTAGATATTTGGGAGG 648
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      381  AGTACGGTAGGGGCAGAGGGAATTTCCGGTGGAGCGGTGAAATGCTAGAGATCGGAAAG 440
QY      649  AACACCAAGTGGCGAAGGCGCTCACTGGCTGCTGATCTACGCTGAGGTGCGGAACCGTGG 708
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      441  AACACCAAGTGGCGAAGGCACTCTGCTGGCGCGACACTGACACTGAGAGACGAAAGCTAGG 500
QY      709  GGACCAACAGGATAGTATACCTGCTGAGTACCGCCGTAACCGTAAACGATGAATCCACACGTC 768
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      501  GGAGCGAATGGGATAGATACCCAGTAGTCTTACCGCTAAACGATGATATAGTGGCGT 560
QY      769  GGCA--AGCATGCTTGTGCTGCTCACACCTAACGGATTAAAGCATTCGCCCTGGGGAGTAC 826
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      561  GTGCTATCGACCCGTCAGTGTCTAGCTAACGGTTAAGTATCCCGCTGGGAGTAC 620
QY      827  GGTGCGAAGATTAACACTCAAAAGGAATTTAGCGGGGCGCCGACAAAGCGGTGAGCATGTG 886
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      621  GTTCGCAAGATTAACACTCAAAAGGAATTTAGCGGGGCGCCGACAAAGCGGTGAGCATGTG 680
QY      887  GTTTAATTCGAAGCAACCGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAG 946
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      681  GTTTAATTCGATGCAAAAGCAAGAACCTTACCAAGGCTTGACATCCCGGAAATCCTCTTG 740
QY      947  AGATTTCAGCTTTCTGTAAGAGACCTGCACACAGTGTGCTGATGCTGTCGTCGACGCTGT 1006
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      741  AAGAGAGGGGTGCTTCGGGAACCGCGACACAGGTGTGATGCTGTCGTCGACGCTGT 800
QY      1007  GTCGTGAGATGTTTCGGTTAAGTCCGGAACAGGCGCAACCAACGCTCCCTAGTGTCCAGCA 1066
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Db      801  GCCGTAAAGTGTGTTGTTAAGTCCGCAACAGGCGCAACCCCTCGTGTAGTGCCA-CC 859
QY      1067  ATTCAAGTGGGAACCTCATGGAACCTGCGGATGATAGTGGAGGAAGGTGTGGATGAGG 1126
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      860  GTTGAGTTTGAACCCCTGAACAGAGTGCCTGTTAAGCGGAGGAAGGTGAGGATGAGG 919
QY      1127  TCAAGTCTCATGCGCTTACGGGTTGGCTTACACACGCTGCTACAAATGG 1175
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      920  TCAAGTCAATCATGCCCCCTTATGCCCCGCGCACACACGCTGCTATCATGG 968

RESULT 11
BZ450751
LOCUS      BZ450751                1077 bp    DNA        linear    GSS 13-DEC-2002
DEFINITION BONKQ63TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONKQ63,
genomic survey sequence.
ACCESSION BZ450751
VERSION   BZ450751.1 GI:26721334
KEYWORDS  GSS.
SOURCE    Brassica oleracea
ORGANISM  Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 1077)
AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE     Whole genome shotgun sequencing of Brassica oleracea
JOURNAL   Unpublished
COMMENT   Other_GSSs: BONKQ63TF
          Contact: Chris Town
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA.
          Tel: 301-838-3523
          Fax: 301-838-0208
          Email: cdtown@tigr.org
          DNA is from a doubled haploid provided by Tom Osborn.
          Seq primer: TR
          Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..1077
                     /organism="Brassica oleracea"

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QY	1229	AACTCGAGGCGATGAAGTTGGAAATCGTCTAGTAAATCGCGAACAG-CATCGCGGGTGAAT	1287
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QY	1288	ACGTTCCCGGGCGCTTGTACACACCGCCCGCTACACCATCGGAGTTGGTTCTACCCGACGA	1347
Db	967	TGTTCCCGGGCGCTTGTACACACCGCCCGCTACACCATCGGAGCTGCGCATGCCGAAAG	1026
QY	1348	CGNTGGCTTAACCTTCGGGGGCGACGGCCACCGGTAGGATACGCCACTGG	1398
Db	1027	TGCTACCTTAACCCGAGGAGGGGTGCGGAAGCAGGCTAGTACTGG	1077
RESULT 12			
BH647750/c			
LOCUS	BH647750	1054 bp	DNA linear GSS 19-FEB-2002
DEFINITION	BOMND31TR BO_2_3_KB Brassica oleracea genomic clone BOMND31,		
ACCESSION	BH647750		genomic survey sequence.
VERSION	BH647750.1	GI:18705298	
KEYWORDS	GSS.		
SOURCE	Brassica oleracea		
ORGANISM	Brassica oleracea		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spezmatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids		
TITLE	; eurosids II; Brassicales; Brassicaceae; Brassica.		
JOURNAL	1 (bases 1 to 1054)		
COMMENT	Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished Contact: Chris Town		
FEATURES			
source	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA.		
	Tel: 301-838-3523		
	Fax: 301-838-0208		
	Email: cdtown@tigr.org		
	DNA is from a doubled haploid provided by Tom Osborn.		
	Seq primer: TR		
	Class: sheared ends.		
	Location/Qualifiers		
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	/clone="BOMND31"		
	/clone_lib="BO_2_3_KB"		
	/note="Vector: pHOS1; Site:1: BstXI; 2-3 kb sheared		
	genomic DNA inserted into pHOS1 using BstXI linkers"		
BASE COUNT	201 a 334 c 263 g 256 t		
ORIGIN			
Query Match	38.4%;	Score 557;	DB 28; Length 1054;
Best Local Similarity	74.4%;	Pred. No. 1.7e-142;	
Matches	778;	Conservative 0;	Mismatches 241; Indels 27; Gaps 5;
QY	432	AGGCCCCGGCTAACTTCGGTGCACAGCGCGGTAAATACGAGGGGCTAGCGTTGTCG	491
Db	1054	AAGCATCGCTAACTCTGTGCAGCAGCGCGGTAAATACAGAGGATGAAGCGTTATCCG	995
QY	492	GAATTACTTGGCGTAAAGCGCACGTAGCGCGGACTGGAAGTCAGAGGTGAATCCACGG	551
Db	994	GAATGATTTGGCGTAAAGCGTCTGTAGTGG-CTTTTAACTCCCGCTCAATCCACGG	936
QY	552	CTCAACCTTGGAACTTCGTTTGAAGTATCATCGTCTGGAGTTTCGAGAGGCTGAGTGAAT	611
Db	935	CTCAACCTTGGACAGCGGTGGAATACCACTACCAAGCTTGAGTACGGTAGGGCAGAGGAAT	876
QY	612	TCCGAGTGTAGAGGTGAATTCGTATAGATATTCGAGGAGAACACCACTGGCGAGCGGCTC	671
Db	875	TTCCGGTGGCGGTGAATGCGTAGAGATCGGAAAGACCAACCAACGGGCAAGACACTCT	816

QY 672 ACTGGCTGCTACTGACGCTGAGTGGGAAGCGTGGGAGCAACAGGATAGATACCC 731
 Db 815 GTGGCCGACACATGACATGAGAGAGCAAGATAGGGAGCGAATGGATAGATACCC 756
 QY 732 TGTAGTCCACGCGCTAAAGCATGAATGCCAGAGC--TCGGCAAGCATGCTTGCCTGT 789
 Db 755 CAGTAGTCTAGCCGTAACGATGGATAGGCGTGTGCGTATCGACCCGTCAGTCG 696
 QY 790 CACACCTTAAGCATTCCGCTGGGAGTACGCTGCGAAGATTAAACCTCAAG 849
 Db 695 TGTAGCTAACGCGCTTAAGTATCCGCTGGGAGTACGCTTCCGAAGATGAACCTCAAG 636
 QY 850 GAATTGACGGGCGCCGACAGCGGTGGAGCATGGTTTAATTCGAAGCAAGCCGAG 909
 Db 635 GAATTGACGGGCGCCGACAGCGGTGGAGCATGGTTTAATTCGAAGCAAGCCGAG 576
 QY 910 AACTTACCAACCTTTGACATGCGAGCGCTGGAGAGATTGAGCTTTCTCGTAAGAGA 969
 Db 575 AACTTACCAAGGCTTGACATGCGGAGATCTCTTGAAGAGAGGGGCTTCCGGA 516
 QY 970 CCGTGCACAGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1029
 Db 515 CGCGGACACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 456
 QY 1030 CGGACAGGCGCAACCCAGCTCCCTAGTTGGCAGCAATTCAGTTGGGAACTCTATGAA 1089
 Db 455 CGCAACGAGCGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 397
 QY 1090 ACTGCCGATGATAAGTCGAGGAGGTGCTGATGACGTCAAGTCTCATGGGCTTACGG 1149
 Db 396 ACTGCCGATGATAAGTCGAGGAGGTGCTGATGACGTCAAGTCTCATGGGCTTACGG 337
 QY 1150 GTTGGGCTACACAGCTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
 Db 336 CCGTGGGCGACACAGCTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 277
 QY 1189 -TTAATCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1247
 Db 276 CTAACTCCAAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 217
 QY 1248 GGAATGCTAGTATCCGGAACAG-CATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1306
 Db 216 GGAATGCTAGTATCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 157
 QY 1307 ACACCGCCCTCACACCATGGAGTGGTTCTTACCCAGCAGCTGCTGCTGCTGCTGCTGCTGCT 1366
 Db 156 ACACCGCCCTCACACCATGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 97
 QY 1367 GGCAGGCGCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1426
 Db 96 AGGGGGGTGCGGAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 37
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 Db 36 GGAAGTCCGCTGGAACCTGCTT 11

RESULT 13
 BH656222/c
 LOCUS
 DEFINITION
 genomic survey sequence.

BH656222
 BH656222.1 GI:18714532
 GSS.

Brassica oleracea
 Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 1031)
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea

JOURNAL Unpublished
 COMMENT Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
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 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
 FEATURES
 Location/Qualifiers
 source
 1..1031
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BOMJ286"
 /clone_lib="BO_2_3_KB"
 /note="Vector: PHOS1; Site1: BstXI; 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers."
 BASE COUNT 198 a 327 c 250 g 256 t
 ORIGIN

Query Match 37.9%; Score 549.8; DB 28; Length 1031;
 Best Local Similarity 73.9%; Pred.No.1.6e-140;
 Matches 762; Conservative 0; Mismatches 242; Indels 27; Gaps 4;
 QY 297 ACTCCTACGGGAGGAGCAGTGGGAATCTTATAGCAATGGGGCAACCTGATCTAGCCCA 356
 Db 1031 ACTCCTACGGGAGGAGCAGTGGGAATCTTCCGCAATGGGGCAACCTGATCTAGCCCA 972
 QY 357 TGGCGCGTGTGATGAAGGCTTAGGGTTGTAAGCTCTTTCAAGCTGCGGAAGA--TAAT 414
 Db 971 TGGCGCGTGTGATGAAGGCTTAGGGTTGTAAGCTCTTTCCAGAGAAGAAGCAAT 912
 QY 415 GACGTACACAGAGAGAGCCCGGCTTAACCTCCGTCAGCAGCAGCGCGGTATACGGAG 474
 Db 911 GACGTATCTGGGAATTAAGCATCGGCTAACTCTGTCCAGCAGCGCGGTATACAGAG 852
 QY 475 GGGCTACGCTGTTCGGAATTAACCTGAGGCGTAAAGCAGCAGTGGGCACTGGAAGTCA 534
 Db 851 GATGCAAGCTTATCCGGAATGATGGGCGTAAAGGCTGTGTAGTGGCTTTTAACTTC 792
 QY 535 GAGGTGAATCCAGGGCTCAACCTTGAAGCTGCTTTGAAACTATCATCTGAGTGGAGTTCG 594
 Db 791 GCCGTCAATCCAGGGCTCAACCTTGAAGCTGCTTTGAAACTATCATCTGAGTGGAGTTCG 732
 QY 595 AGAGAGTGTGAGTGGGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAGACAC 654
 Db 731 GTAGGGCAGAGGGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAGACAC 672
 QY 655 AGTGGCAAGGCGGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
 Db 671 AACGCGAAGACACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
 QY 715 AACAGGATTAGTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772
 Db 611 AATGGATTAGTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
 QY 773 AGCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832
 Db 551 ATGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
 QY 833 AAGATTAAACTCAAAAGGAATGACGGGGCGCCGACACAGCGGTGAGCATGTGTTTAA 892
 Db 491 AAGATTAAACTCAAAAGGAATGACGGGGCGCCGACACAGCGGTGAGCATGTGTTTAA 432
 QY 893 TTCGAAGCAAGCGCAGAACCTTACCAACCTTTGATGATGGAGGAGCGGTGAGGAGATTC 952
 Db 431 TTCGATGCAAGCGCAGAACCTTACCAACCTTTGATGATGGAGGAGCGGTGAGGAGATTC 372
 QY 953 AGCTTTCGTAAGAGACCTGCACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1012
 !!

[illegible]

